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80      61      2.4      982      17      AF011221
81      61      2.4      1080      14      BM810567
82      61      2.4      1189      12      BG611961
83      60      2.3      490      17      BH152886
84      59      2.3      226      12      BF854329
85      59      2.3      263      9      AA825185
86      59      2.3      312      17      AF166285
87      59      2.3      317      9      AA573000
88      59      2.3      349      10      AW770050
89      59      2.3      379      17      AQ580711
90      59      2.3      382      17      AA219031
91      59      2.3      383      12      BF755195
92      59      2.3      409      13      BG952898
93      59      2.3      420      9      AA835931
94      59      2.3      422      9      AA743968
95      59      2.3      440      17      B17487
96      59      2.3      447      17      AQ038575
97      59      2.3      518      17      AQ412294
98      59      2.3      524      12      BF737749
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100     59      2.3      592      14      BQ272418

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ALIGNMENTS

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RESULT 1
AL541041      877 bp      mRNA      linear      EST 16-FEB-2001
LOCUS         AL541041 LTT FL002_P11 Homo sapiens cDNA clone CSDB005YK23 5 prime
DEFINITION    AL541041 LTT FL002_P11 Homo sapiens cDNA clone CSDB005YK23 5 prime
ACCESSION     AL541041
VERSION       AL541041.1 GI:12871733
KEYWORDS      EST.
SOURCE        human.
ORGANISM      Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE     1 (bases 1 to 877)
AUTHORS      Li W.B., Gruber C., Jessee J. and Polayes D.
TITLE        Full-length cDNA libraries and normalization
JOURNAL       Unpublished (2001)
COMMENT       Genoscope
               Genoscope - Centre National de Sequencage
               BP 191 91006 Evry cedex - France
               Email: seqref@genoscope.cns.fr, web : www.genoscope.cns.fr.

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FEATURES
source
1..877
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CSDB005YK23"
/clone_11b="LTT_FL002_P11"
/lab_host="DH10B"
/notes="Organ: placenta; Vector: pCMVSPORT 6; 1st strand
cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-stranded cDNA was digested with Not I
and cloned into the Not I and Eco RV sites of the
pCMVSPORT 6 vector. Library was constructed by Life
Technologies. Contact : Feng Liang Life Technologies, a
division of Invitrogen 9800 Medical Drive Rockville
, Maryland 20850, USA Fax : (1) 301 610 8371 Email :
filiang@life.com URL :
http://fulllength.invitrogen.com"

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BASE COUNT    192 a      262 c      251 g      170 t      2 others
ORIGIN

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Query Match      30.3%; Score 778; DB 9; Length 877;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 828; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY      29      CAAGACCCCAAGCCTGTCTCTGTGACAGAGCTCAAGAGGCGCTGGGCTTCCCTCC 88
Db      1      CAAGACCCCAAGCCTGTCTCTGTGACAGAGCTCAAGAGGCGCTGGGCTTCCCTCC 60

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QY      89      TGGCTCGGCTGTGCTCTGGAGGGGTTCCCAAGTCCAGATCCCTTAAGAGATGGGGCAGC 148
Db      61      TGGCTCGGCTGTGCTCTGGAGGGGTTCCCAAGTCCAGATCCCTTAAGAGATGGGGCAGC 120
QY      149      TGAATCATCCCTGTGTTCAAACTGCTGACAGACAGATGCTAGCTAACCAACCA 208
Db      121      TGAATCATCCCTGTGTTCAAACTGCTGACAGACAGATGCTAGCTAACCAACCA 180
QY      209      CACTTACCTCTCTCCCTGAAAGATCTCCAGCTGAGAGAGATTCCTGGTCTCTAGACCA 268
Db      181      CACTTACCTCTCTCCCTGAAAGATCTCCAGCTGAGAGAGATTCCTGGTCTCTAGACCA 240
QY      269      AGGACACTGACACTTCCAGAGAGGCGCCCAAGCCCTTAAGCTGTCAGCAGAGCATG 328
Db      241      AGGACACTGACACTTCCAGAGAGGCGCCCAAGCCCTTAAGCTGTCAGCAGAGCATG 300
QY      329      GCTTCAGCAGAGCTGTCTTCCAGGCTTTGATGACAAACATTTCCCTGATGATGT 388
Db      301      GCTTCAGCAGAGCTGTCTTCCAGGCTTTGATGACAAACATTTCCCTGATGATGT 360
QY      389      GCTTCAGAGTCTCTGCTGAGGAACAATGGAAGTCTGCCAGCAGAGAAATCTTGC 448
Db      361      GCTTCAGAGTCTCTGCTGAGGAACAATGGAAGTCTGCCAGCAGAGAAATCTTGC 420
QY      449      CAAGCCCAAGCTTGAATCTCTCTGTCAGGCGCAGGACCTGTGACCATGAGAGAGAGA 508
Db      421      CAAGCCCAAGCTTGAATCTCTCTGTCAGGCGCAGGACCTGTGACCATGAGAGAGAGA 480
QY      509      GAAGCAAGGCGCAGGCGCTTGGGCGAGTTCCCGGCGAGTGCGCCGCGCAGAGTGT 568
Db      481      GAAGCAAGGCGCAGGCGCTTGGGCGAGTTCCCGGCGAGTGCGCCGCGCAGAGTGT 540
QY      569      CGCTGAGACTCGGGAGGACCATTTGACATCTGCTGAGAGATGAGATGAGTGAAGGTC 628
Db      541      CGCTGAGACTCGGGAGGACCATTTGACATCTGCTGAGAGATGAGATGAGTGAAGGTC 600
QY      629      TGTCTGAAGTCTCAGCAGAGAGTATTAACATCCAGGCTCAGCTGGCCCAAGTCTCC 688
Db      601      TGTCTGAAGTCTCAGCAGAGAGTATTAACATCCAGGCTCAGCTGGCCCAAGTCTCC 660
QY      689      ATGGGTGCTGTATGAGGCGCTGAGCGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAG 748
Db      661      ATGGGTGCTGTATGAGGCGCTGAGCGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
QY      749      GGAACCTTGAGAGGCGCTTCTCATCCGGGAGGCGCAGAGACGAGAGAGGCTTACTCTC 808
Db      721      GGAACCTTGAGAGGCGCTTCTCATCCGGGAGGCGCAGAGACGAGAGAGGCTTACTCTC 780
QY      809      TGTCTGCTCGGCTGAGGCGCTTCTCATCCGGGAGGCGCAGAGAGGCTTACTCTCTC 857
Db      781      TGTCTGCTCGGCTGAGGCGCTTCTCATCCGGGAGGCGCAGAGAGGCTTACTCTCTC 829

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RESULT 2
B0052308      1002 bp      mRNA      linear      EST 29-MAR-2002
LOCUS         B0052308
DEFINITION    AGENCOURT_6868571 NIH_MGC_106 Homo sapiens cDNA IMAGE:593542
ACCESSION     B0052308
VERSION       B0052308.1 GI:19811648
KEYWORDS      EST.
SOURCE        human.
ORGANISM      Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

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REFERENCE     1 (bases 1 to 1002)
AUTHORS      NIH-MGC http://mgc.nci.nih.gov/.
TITLE        National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL       Unpublished (1999)
COMMENT       Contact: Robert Strauberg, Ph.D.
               Email: cga@bs-riemail.nih.gov
               Tissue Procurement: Dr. Daniel McVicar, DBS/NCI

```

CDNA library Preparation: Rubin Laboratory
 CDNA library Arrayed by: the I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.lnl.gov>
 Plate: LNCM218 row: d column: 23
 High quality sequence stop: 670.

FEATURES

source

1..1002

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:5933542"

/clone_lib="NIH MGC 106"

/tissue_type="natural killer cells, cell line"

/lab_host="DH10B (phage-resistant)"

/note="Organ: blood; Vector: pMT7; Site: 1; XhoI; Site 2:

EcoRI; CDNA made by oligo-dT priming. Directionally cloned

into EcoRI/XhoI sites using the following 5' adaptor:

GGCAGAG(G). Library constructed by Ling Hong in the

laboratory of Gerald M. Rubin (University of California,

Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and

Superscript II RT (Life Technologies). Note: this is a

NIH MGC library."

BASE COUNT 221 a 296 c 288 g 197 t
 ORIGIN

Query Match 27.2%; Score 698; DB 14; Length 1002;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 748; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 350 CCAAGCTTGTGATGACAAACCAATTCCTCGATGATGCTGTGAGGCTCTGTAG 409
 Db 31 CCAAGCTTGTGATGACAAACCAATTCCTCGATGATGCTGTGAGGCTCTGTAG 90
 QY 410 GAACAATGGAAGTCTGCCAGCAGAAATTCCTGCCAGCCCAAGCTTGAGTTCT 469
 Db 91 GAACAATGGAAGTCTGCCAGCAGAAATTCCTGCCAGCCCAAGCTTGAGTTCT 150
 QY 470 CTGTCCAAAGCCAGGACCTGTGACATGTGAAGCAGAGAGAGAGAGAGAGAGAG 529
 Db 151 CTGTCCAAAGCCAGGACCTGTGACATGTGAAGCAGAGAGAGAGAGAGAGAGAG 210
 QY 530 CCTGGGCAATTTCCCGGAGGTGGCCCGGCGAGCTGTCCCTGAGACTTGGGGAGCCAT 589
 Db 211 CCTGGGCAATTTCCCGGAGGTGGCCCGGCGAGCTGTCCCTGAGACTTGGGGAGCCAT 270
 QY 590 TGACCATCTCTCTGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 649
 Db 271 TGACCATCTCTCTGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 330
 QY 650 AGTTTAAATCCCAAGCTTCAAGTGGCCAAAGTCTCCCATGGGTGCTGTATGAGGCC 709
 Db 331 AGTTTAAATCCCAAGCTTCAAGTGGCCAAAGTCTCCCATGGGTGCTGTATGAGGCC 390
 QY 710 TGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 769
 Db 391 TGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 450
 QY 770 TCATCCGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 829
 Db 451 TCATCCGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 510
 QY 830 CTGATCTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 889
 Db 511 CTGATCTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 570
 QY 890 ACATCTCAACGGGCTCACTTCCCTCACTTCCAGGCTCTGTGAGCATTAATCTTGAGC 949
 Db 571 ACATCTCAACGGGCTCACTTCCCTCACTTCCAGGCTCTGTGAGCATTAATCTTGAGC 630
 QY 950 TGGCGATGACATCTGCTGCTACTCAAGAGAGCCCTGTGTCTCTCAAGAGGCTGGCCGC 1009

Db 631 TGGCGATGACATCTGCTGCTACTCAAGAGAGCCCTGTGTCTCTCAAGAGGCTGGCCGC 690
 QY 1010 TCCCTGGCAAGAGATATACCTTACTGTGACTGTGACAGAGACCACTCAATGGAAG 1069
 Db 691 TCCCTGGCAAGAGATATACCTTACTGTGACTGTGACAGAGACCACTCAATGGAAG 750
 QY 1070 AGCTGGAGAGCTCCCTGCTGTTTCTGAA 1098
 Db 751 AGCTGGAGAGCTCCCTGCTGTTTCTGAA 779

RESULTS

3

Bg677567

LOCUS

DEFINITION

Bg677567

VERSION

KEYWORDS

SOURCE

ORGANISM

human

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

1 (bases 1 to 794)

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgaab@tmail.nih.gov

Tissue Procurement: James Cleaver, M.D.

CDNA Library Preparation: Life Technologies, Inc.

DNA sequencing by: Invitrogen, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL at:

<http://image.lnl.gov>

Plate: LLM10601 row: d column: 05

High quality sequence stop: 790.

Location/Qualifiers

1..794

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:4748884"

/clone_lib="NCI CGAP Skin4"

/tissue_type="squamous cell carcinoma"

/lab_host="DH10B (T1 phage-resistant)"

/note="Organ: skin; Vector: PCMV-SPORE6; Site 1: NotI;

Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.

Average insert size 1.5kb. Library constructed by Life

Technologies. Note: this is a NCI CGAP library."

BASE COUNT 192 a 229 c 212 g 161 t

ORIGIN

Query Match 24.6%; Score 631; DB 12; Length 794;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 631; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 946 GAGTGGCCGATGACATCTGCTGCTCACTCAAGAGCCCTGTGTCTGTGAGAGGCTGGC 1005
 Db 17 GAGTGGCCGATGACATCTGCTGCTCACTCAAGAGCCCTGTGTCTGTGAGAGGCTGGC 76
 QY 1006 CCGCTCCCTGGAGAGATATACCTTACTGTGACTGTGAGAGAGAGAGAGAGAGAGAG 1065
 Db 77 CCGCTCCCTGGAGAGATATACCTTACTGTGACTGTGAGAGAGAGAGAGAGAGAGAG 136
 QY 1066 AAGAGAGTGAAGAGTCCCTGCTTCTGAGAGTCCCAAGAGAGAGAGAGAGAGAGAG 1125
 Db 137 AAGAGAGTGAAGAGTCCCTGCTTCTGAGAGTCCCAAGAGAGAGAGAGAGAGAGAG 196
 QY 1126 AGTGAAGGCTCTCGGAGAGTCCCTCACTTCAATCAAGCTGATGACAGAGCTGTCT 1185
 Db 197 AGTGAAGGCTCTCGGAGAGTCCCTCACTTCAATCAAGCTGATGACAGAGCTGTCTCT 256

Qy	1186	TTGATGATGCTTAAGGCCCAAGAGAGAGCCCAAAAGGAAACCAAGGCTGACACCTTGA	1245
Db	257	TTGATGATGCTTAAGGCCCAAGAGAGAGCCCAAAAGGAAACCAAGGCTGACACCTTGA	316
Qy	1246	ACCCCAATTCAGAGCTCTCTGGGACACCCCAAGGCAAGGCTGTGCACTACGGAGAGAGGCT	1305
Db	317	ACCCCAATTCAGAGCTCTCTGGGACACCCCAAGGCAAGGCTGTGCACTACGGAGAGAGGCT	376
Qy	1306	GGGACACAGAGGTGCATCTAGAGGTCCCACTGTGACCTTGTCTTCTCTCTTACGCTT	1365
Db	377	GGGACACAGAGGTGCATCTAGAGGTCCCACTGTGACCTTGTCTTCTCTCTTACGCTT	436
Qy	1366	TGAGAGTACACTCTCTCTCTAGTGCATGATCCGACCTGTGGACCTCTGTATGTCAGATGC	1425
Db	437	TGAGAGTACACTCTCTCTCTAGTGCATGATCCGACCTGTGGACCTCTGTATGTCAGATGC	496
Qy	1426	AAGAGAGGTGGGACCAAGGCCCAAGGGTTCCAAAAAGAGATTAAGCTCTGTGGGGGTCTTGA	1485
Db	497	AAGAGAGGTGGGACCAAGGCCCAAGGGTTCCAAAAAGAGATTAAGCTCTGTGGGGGTCTTGA	556
Qy	1486	CCTAGTATGTTCTTTGAGTTTGGGGTTTCCAGTACCATCTTGATATGCCCTGTGTTAGCC	1545
Db	557	CCTAGTATGTTCTTTGAGTTTGGGGTTTCCAGTACCATCTTGATATGCCCTGTGTTAGCC	616
Qy	1546	CCATTCTACATCCCGACCAATTAAACAAGGCC	1576
Db	617	CCATTCTACATCCCGACCAATTAAACAAGGCC	647

[illegible]

REFERENCE	1 (bases 1 to 986)
AUTHORS	NIH-MGC http://imgc.nhl.nih.gov/
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D.

Tissue Procurement: Dr Daniel McVicar, DBS/NCI
 cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Place: LRCM2125 row: 1 column: 12
 High quality sequence stop: 515.

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FEATURES
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Location/Qualifiers
1..986
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="536339"
/clone_id="N1H.MGC.106"
/tissue_type="natural killer cells, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: blood; Vector: pGEM7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming, directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GCCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a N1H.MGC library."
BASE COUNT
211 a 291 c 276 g 207 t 1 others

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ORIGIN
 Query Match 24.5%; Score 629; DB 14; Length 986;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 629; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	137	GCATGGGGGACGCTGATCCATCCCTGGGTATACAACTGCTGACTCAGACAGATGCTGAGC	196
Db	1	GGATGGGGGACGCTGATCCATCCCTGGGTATACAACTGCTGACTCAGACAGATGCTGAGC	60
Qy	197	TACCCAAACCAACCTTAGCTCTCCCTGGAAAGTACCTCCAGGCTGAGAGATCTGGGT	256
Db	61	TACCCAAACCAACCTTAGCTCTCCCTGGAAAGTACCTCCAGGCTGAGAGATCTGGGT	120
Qy	257	GTCTTAGAGCAACAGGACACTGGGACACTTCCAGAGGGGCCCCCAAGCCCTAACCTGTCC	316
Db	121	GTCTTAGAGCAACAGGACACTGGGACACTTCCAGAGGGGCCCCCAAGCCCTAACCTGTCC	180
Qy	317	AGCCAGAGCATGGGTCTCAGCAGAGAGGTGTCTCCCAAGCTTTGATGACAAACCAATTTC	376
Db	181	AGCCAGAGCATGGGTCTCAGCAGAGAGGTGTCTCCCAAGCTTTGATGACAAACCAATTTC	240
Qy	377	CCTGATGATGTGCTTCTGAGTGCTCTGTCGAGAAACAATGGAGAACTTGCCACAGAA	436
Db	241	CCTGATGATGTGCTTCTGAGTGCTCTGTCGAGAAACAATGGAGAACTTGCCACAGAA	300
Qy	437	GAAAAATCTCGGCAAGCCCAAGCTTGAGATTCTCTCTCAAGGCAAGGACCTGTGACCA	496
Db	301	GAAAAATCTCGGCAAGCCCAAGCTTGAGATTCTCTCTCAAGGCAAGGACCTGTGACCA	360
Qy	497	TGGAAAGAGAGAAAGCAAGGCCACAGCCGTGGCCCTGGGCAATTTCCGGCAGGTGGCC	556
Db	361	TGGAAAGAGAGAAAGCAAGGCCACAGCCGTGGCCCTGGGCAATTTCCGGGAGGTGGCC	420
Qy	557	CGGCGAGCTGTGCGCTGAGACTCGGSGAGACCAATTGACACATGCTCTGAGGATGAGACT	616
Db	421	CGGCGAGCTGTGCGCTGAGACTCGGSGAGACCAATTGACACATGCTCTGAGGATGAGACT	480
Qy	617	GGTGGAGGCTGCTCTGAAAGTCTCAGGCAAGAGATATAACATCCCAAGGTCCACCTGG	676
Db	481	GGTGGAGGCTGCTCTGAAAGTCTCAGGCAAGAGATATAACATCCCAAGGTCCACCTGG	540
Qy	677	CCAAAGCTCCCATGGGTGCTGTATGAGGCGCTGACAGGAGAAAGCAAGAACTGCG	736
Db	541	CCAAAGCTCCCATGGGTGCTGTATGAGGCGCTGACAGGAGAAAGCAAGAACTGCG	600
Qy	737	TGTTCTTAACCTGGAGACCTGGAGGGGCC	765
Db	601	TGTTCTTAACCTGGAGACCTGGAGGGGCC	629

RESULT 5	BQ054281				
LOCUS	BQ054281				
DEFINITION	ABENICOURT_6830234 NIH_MGC_106 Homo sapiens cDNA clone IMAGE:5936362				
ACCESSION	BQ054281	1020 bp	mRNA	linear	EST 29-MAR-2002
VERSION	BQ054281				
KEYWORDS	BQ054281.1	GI:19813621			
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS	1 (bases 1 to 1020)				
TITLE	NIH-MGC http://mgc.nci.nih.gov/ .				
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)				
COMMENT	Unpublished (1999)				
	Contact: Robert Strausberg, Ph.D.				
	Email: cgapbs-remail.nih.gov				
	Tissue Procurement: Dr. Daniel McVicar, DBS/NCI				
	cDNA Library Preparation: Rubin Laboratory				
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)				
	DNA Sequencing by: National Bioscience Corporation				

Qy	567	GTCCGTGAGACTCGGGGAGCCATTGACCATCGTCTCTGAGAGATGGAATCTGTGACGGT	626
Db	241	GTCCGTGAGACTCGGGGAGCCATTGACCATCGTCTCTGAGAGATGGAATCTGTGACGGT	300
Qy	627	GCTGTCTGAGTCTCAGGCAGAGATTAACATCCCAAGCTCCAGTGGCCAAAGTTC	686
Db	301	GCTGTCTGAGTCTCAGGCAGAGATTAACATCCCAAGCTCCAGTGGCCAAAGTTC	360
Qy	687	CCATGGGTGCTCTTAAGAGGCGCTGAGCAGAGGAGAAAGCAGAGGAACTGCTGTGTTACC	746
Db	361	CCATGGGTGCTCTTAAGAGGCGCTGAGCAGAGGAGAAAGCAGAGGAACTGCTGTGTTACC	420
Qy	747	TGGGAAACCTGAGAGGGGCGCTTCTCAATCCGGGAGAGCAGAACCCAGAGAGGCTCTTAATC	806
Db	421	TGGGAAACCTGAGAGGGGCGCTTCTCAATCCGGGAGAGCAGAACCCAGAGAGGCTCTTAATC	480
Qy	807	TCTGTCAAGTCGCGCTTCAAGCGCCCTCGATCTCTGGAGCCGGATCAGACCTAACAGATCCA	866
Db	481	TCTGTCAAGTCGCGCTTCAAGCGCCCTCGATCTCTGGAGCCGGATCAGACCTAACAGATCCA	540
Qy	867	CTGCGCTTGAGAAAGTGGCTGTATCAATCCACCGGCGTACCTTCCCTCATCCAGAGC	926
Db	541	CTGCGCTTGAGAAAGTGGCTGTATCAATCCACCGGCGTACCTTCCCTCATCCAGAGC	600
Qy	927	CCCTGG 931	
Db	601	CCCTGG 605	

RESULT 7	AL568702/c	854 bp	MRNA	linear	EST 16-FEB-2001
LOCUS	AL568702/c				
DEFINITION	AL568702 L11_F1002_P11 Homo sapiens cDNA clone CSDBE005K23 3 prime				
ACCESSION	AL568702				
VERSION	AL568702.1				
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Bukacinski, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS	Li, W. B., Gruber, C., Jesse, J. and Polayes, D.				
TITLE	Full-length cDNA libraries and normalization				
JOURNAL	Unpublished (2001)				
COMMENT	Contact: Genoscope				

BASE COUNT	ORIGIN	FEATURES
195 a	200 c	236 g
219 t	4 others	

Query Match	23.4%	Score 600;	DB 9;	Length 854;
Best Local Similarity	100.0%	Pred. No. 0;		
Matches 600;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

Oy	1841	TTTTGGAGAGAGAGAGTCTTGAGCCCTTGTTGCCAATGCTGGAGAGTCAAGAGCATCTAG	1900
Db	602	TTTTTTGAGACCGAGAGTCTTGACCTCTTGTCCTCATGCTGGAGTGCMAATGGACGATCTCAG	543
Oy	1901	CTCACTGCACACTCTCATCTCTTGATTCMAACAAATTCCTGCTCAAGCTTCAAGATAG	1960
Db	542	CTCACTGCACACTCCATCTCTTGATTCMAACAAATTCCTGCTCAAGCTTCAAGATAG	483
Oy	1961	CTGGGATTAAGGCGCTACACACACATGCTGGCTAAATTTTTTGTATTTTGTAGTACAT	2020
Db	482	CTGGGATTAAGGCGCTACACACACATGCTGGCTAAATTTTTTGTATTTTGTAGTACAT	423
Oy	2021	GGGGTTTTCACCAATTGGCGACAGCTGTGTGAACTCTGACCTCAAGTATTCACCCAC	2080
Db	422	GGGGTTTTCACCAATTGGCGACAGCTGTGTGAACTCTGACCTCAAGTATTCACCCAC	363
Oy	2081	CTTGGACCTCCCAAGATGTGTGGAAATTACAGGTGTAGCCACCGCACCGACTTACGCTCA	2140
Db	362	CTTGGACCTCCCAAGATGTGTGGAAATTACAGGTGTAGCCACCGCACCGACTTACGCTCA	303
Oy	2141	GATCTCTATTTCATTTTGTGGCTTACCATTTCCTAGCAACACTGAGCTTGCATCTTTGGG	2200
Db	302	GATCTCTATTTCATTTTGTGGCTTACCATTTCCTAGCAACACTGAGCTTGCATCTTTGGG	243
Oy	2201	CCGAATAAAAATAACACTCTTAATGTAGACACACTGACGTGAGGCGACAGCACTCTCAGT	2260
Db	242	CCGAATAAAAATAACACTCTTAATGTAGACACACTGACGTGAGGCGACAGCACTCTCAGT	183
Oy	2261	GCTGGGCGAGGGGATTCAGAAAGTGTCTAAGCCCTCTCCCAAAATGCCAACAAGAGAACCA	2320
Db	182	GCTGGGCGAGGGGATTCAGAAAGTGTCTAAGCCCTCTCCCAAAATGCCAACAAGAGAACCA	123
Oy	2321	CAGCCTACACAAATCTCAGCCCTTGTATTTTCCCTCTGCTCCATTAACAGAAAGAGTCT	2380
Db	122	CAGCCTACACAAATCTCAGCCCTTGTATTTTCCCTCTGCTCCATTAACAGAAAGAGTCT	63
Oy	2381	GCTGGATTCGCTTAAGGATTCAGGAGAGAGAAAGAGGATGGGGGTGGAGGSCACCCCC	2440
Db	62	GCTGGATTCGCTTAAGGATTCAGGAGAGAGAAAGAGGATGGGGGTGGAGGSCACCCCC	3

RESULT	8
LOCUS	AL844325
DEFINITION	AL844325 pool_YT_11b_v_SPD Homo sapiens cDNA, linear EST 30-JUL-2002.
ACCESSION	AL844325
VERSION	AL844325.1 GI:22019105
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 677) Ashcroft,K., Bethel,G., Bye,J.M., Howell,G.R., Huckle,E.J. and Sheridan,E. Homo sapiens EST sequence Unpublished (2002) Contact: The Sanger Centre The Sanger Centre Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK Email: humquerry@sanger.ac.uk Sanger Centre name : scdcl0827.4004895 Homo sapiens EST sequence. This sequence was generated as part of The Wellcome Trust Sanger Institute program to identify and annotate genes in the human genome. Incomplete or unconfirmed genes are experimentally analysed using a variety of cDNA library resources. This sequence was obtained from a PCR product generated from a pool of up to 100,000 cDNA clones derived from pool YT_11b v SPD cDNA library. Further information can be found at http://www.sanger.ac.uk/Teams/Team69/ .
FEATURES	Location/Qualifiers
source	1..677

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/map="20"
/clone_id="pool_YT_11b_v_SPD"
/notes="Organ: breast; Vector: pZERO-1; Site_1: SphI; Site_2: SphI; Ductal carcinoma in situ, high-grade, comedo, from 41 yo female. Library constructed in the laboratory of K. Polyak, M.D., Ph.D. (Dana-Farber Cancer Institute)."
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BASE COUNT 160 a 195 c 154 g 168 t

ORIGIN

Query Match 21.7%; Score 557; DB 9; Length 677;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 677; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1680 TGGGCTGAAGGAAAGAAAGCTGAGATATGTCTTACCGAGACAGATCTGGATG 1739
 Db 1 TGGGCTGAAGGAAAGAAAGCTGAGATATGTCTTACCGAGACAGATCTGGATG 60

QY 1740 GTCCAGGCTCTATGTGACCTCCAGAGAAAGAAAGACTTGGAGACAGTCTGCTCA 1739
 Db 61 GTCCAGGCTCTATGTGACCTCCAGAGAAAGAAAGACTTGGAGACAGTCTGCTCA 120

QY 1800 AATGCCCCCATTTGAGAGCAACAGCCAGCTCTTTCTTTTGTGAGAGAGTCT 1859
 Db 121 AATGCCCCCATTTGAGAGCAACAGCCAGCTCTTTCTTTTGTGAGAGAGTCT 179

QY 1860 TGGGCTGAGGCTGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1919
 Db 180 TGGGCTGAGGCTGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 239

QY 1920 CCTGATTCAGAAATTTCTGCTGAGCTCCAGAAATGAGTGGAGTTCAGAGGCTCA 1979
 Db 240 CCTGATTCAGAAATTTCTGCTGAGCTCCAGAAATGAGTGGAGTTCAGAGGCTCA 299

QY 1980 CCACCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2039
 Db 300 CCACCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 359

QY 2040 CAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2099
 Db 360 CAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 419

QY 2100 GGGATTCAGAGTGAAGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCA 2159
 Db 420 GGGATTCAGAGTGAAGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCA 479

QY 2160 GGGATTCAGAGTGAAGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCA 2219
 Db 480 GGGATTCAGAGTGAAGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCA 539

QY 2220 TCTTAAGTCTAGACACTGAGTGAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCA 2279
 Db 540 TCTTAAGTCTAGACACTGAGTGAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCA 599

QY 2280 AGGTGCTAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2339
 Db 600 AGGTGCTAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 659

QY 2340 CCTTGAATTCCTGCTG 2357
 Db 660 CCTTGAATTCCTGCTG 677

RESULT 9
 AL844312/c 619 bp mRNA linear EST 30-JUL-2002
 LOCUS AL844312 pool_YT_11b_v_SPD Homo sapiens cDNA, mRNA sequence.
 DEFINITION AL844312
 ACCESSION AL844312
 VERSION AL844312.1 GI:22019094
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 619)
 Ashcroft, K., Bethel, G., Bye, J.M., Howell, G.R., Huckle, E.J. and Sheridan, E.
 Homo sapiens EST sequence
 Unpublished (2002)
 CONTACT: The Sanger Centre
 The Sanger Centre
 Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK
 Email: humquery@sanger.ac.uk
 Sanger Centre name: scd10818.400489A
 Homo sapiens EST sequence. This sequence was generated as part of The Wellcome Trust Sanger Institute program to identify and annotate genes in the human genome. Incomplete or unconfirmed genes are experimentally analysed using a variety of cDNA library resources. This sequence was obtained from a PCR product generated from a pool of up to 100,000 cDNA clones derived from pool_YT_11b_v_SPD cDNA library.
 http://www.sanger.ac.uk/Teams/Team69/
 Location/Qualifiers
 1..619
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /map="20"
 /clone_id="pool_YT_11b_v_SPD"
 /note="Organ: breast; Vector: pZERO-1; Site_1: SphI; Site_2: SphI; Ductal carcinoma in situ, high-grade, comedo, from 41 yo female. Library constructed in the laboratory of K. Polyak, M.D., Ph.D. (Dana-Farber Cancer Institute)."

BASE COUNT 133 a 159 c 177 g 150 t

ORIGIN

Query Match 20.2%; Score 519; DB 9; Length 619;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 569; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1085 TCCGTTTCTGAAGCTCCACAGAGGAGAGTCTTCTCAGTGAAGGCTCCGGAGT 1144
 Db 570 TCCGTTTCTGAAGCTCCACAGAGGAGAGTCTTCTCAGTGAAGGCTCCGGAGT 511

QY 1145 CCTCAGCTTCTATCAGCTGATGAGAGGCTGCTCTTTGATATGCTTGGAGGCTC 1204
 Db 510 CCTCAGCTTCTATCAGCTGATGAGAGGCTGCTCTTTGATATGCTTGGAGGCTC 451

QY 1205 AAAGAGAGCCAAAGGAAACCAAGGCTGACACCTTAAGACCCCAATTCAGCTCCTG 1264
 Db 450 AAAGAGAGCCAAAGGAAACCAAGGCTGACACCTTAAGACCCCAATTCAGCTCCTG 391

QY 1265 GGCACCCCAAGAGCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1324
 Db 390 GGCACCCCAAGAGCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 331

QY 1325 AGGTGCTAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1384
 Db 330 AGGTGCTAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 271

QY 1385 TCCAGTGCATATCCACCTGAGCTCTAGTGAAGTGAAGAGAGTGGAGACAGG 1444
 Db 270 TCCAGTGCATATCCACCTGAGCTCTAGTGAAGTGAAGAGAGTGGAGACAGG 211

QY 1445 CCAGGTTTCCAAAAGAAATAGCCTCTGAGGAGTCTGACCTAGTATGTTGTTGAGATT 1504
 Db 210 CCAGGTTTCCAAAAGAAATAGCCTCTGAGGAGTCTGACCTAGTATGTTGTTGAGATT 151

QY 1505 TGGGTTTCCAGTACATGAGTGAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1564
 Db 150 TGGGTTTCCAGTACATGAGTGAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 91

QY 1565 TTAACAGAGCCCAACCAAGGTAGAAACAACCTTGAAGTCAAGAGAAAGTCAATTT 1624
 Db 90 TTAACAGAGCCCAACCAAGGTAGAAACAACCTTGAAGTCAAGAGAAAGTCAATTT 31

QY 1625 CAGAAATCTACAGTCTGTTGAGCAC 1654
 Db 30 CAGAAATCTACAGTCTGTTGAGCAC 1
 RESULT 10
 LOCUS AL844308/c 642 bp mRNA linear EST 30-JUL-2002
 DEFINITION AL844308 pool_AK_11b_v_SPD Homo sapiens cDNA, mRNA sequence.
 ACCESSION AL844308
 VERSION AL844308.1 GI:22019090
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 642)
 Ashcroft, K., Bethel, G., Bye, J.M., Howell, G.R., Huckle, E.J. and
 Sheridan, E.
 Homo sapiens EST sequence
 Unpublished (2002)
 Contact: The Sanger Centre
 The Sanger Centre
 Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK
 Email: humquery@sanger.ac.uk
 Sanger Centre name : sccid10816.400489A
 Homo sapiens EST sequence. This sequence was generated as part of
 The Wellcome Trust Sanger Institute program to identify and
 annotate genes in the human genome. Incomplete or unconfirmed genes
 are experimentally analysed using a variety of cDNA library
 resources. This sequence was obtained from a PCR product generated
 from a pool of up to 100,000 cDNA clones derived from
 pool_AK_11b_v_SPD cDNA library. Further information can be found at
 http://www.sanger.ac.uk/Teams/teams69/.
 Location/Qualifiers
 1. 642
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /map="20"
 /clone_lib="pool_AK_11b_v_SPD"
 /note="Organ: breast; Vector: pZERO-1; Site: 1; SphI;
 Site_2: SphI; Ductal carcinoma in situ, high-grade, comedo
 , from 41 yo female. Library constructed in the laboratory
 of K. Polyak, M.D., Ph.D. (Dana-Farber Cancer Institute)."
 BASE COUNT 140 a 164 c 181 g 157 t
 ORIGIN
 Query Match 20.1% Score 515; DB 9; Length 642;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 515; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1085 TCTCTGTTTCTGAGCTGCAACAGGAGAGATCTTCTCACTGAGGCTCTCGGAGT 1144
 Db 588 TCTCTGTTTCTGAGCTGCAACAGGAGAGATCTTCTCACTGAGGCTCTCGGAGT 529
 QY 1145 CCTCAGCTTCTACATCAGCTGAATGAGAGAGCTCTTTGATGATGCTTGAAGCC 1204
 Db 528 CCTCAGCTTCTACATCAGCTGAATGAGAGAGCTCTTTGATGATGCTTGAAGCC 469
 QY 1205 AAGGAGAGGCAAAAGGAAACCAAGGTGACACTTAGAACCCCAATTAGCTTCTG 1264
 Db 468 AAGGAGAGGCAAAAGGAAACCAAGGTGACACTTAGAACCCCAATTAGCTTCTG 409
 QY 1265 GGCACCCAGAGCAAGGCTGTGCACTAGGAGAGGAGGTGGACACAGAGTGCATCT 1324
 Db 408 GGCACCCAGAGCAAGGCTGTGCACTAGGAGAGGAGGTGGACACAGAGTGCATCT 349
 QY 1325 AGGGTCCACCTGTAACCTTGTCTTCTCTTTAGCCTTGAAGTCACTTCTCT 1384
 Db 348 AGGGTCCACCTGTAACCTTGTCTTCTCTTTAGCCTTGAAGTCACTTCTCTCT 289
 QY 1385 TCCAGTGCATGATCCACCTGAGACTTGTGAGTGCAGAGAGAGTGGAGCCAGG 1444

Db 288 TCCAGTGCATGATCCACCTGAGCCTCTTAGTGCAGTGCAGAAAGTGGACCAAGG 229
 QY 1445 CCAGGTTCCAAAAGAGATTAAGCTCTGAGGAGGCTGACCTAGTATTGTTGAGTT 1504
 Db 228 CCAGGTTCCAAAAGAGATTAAGCTCTGAGGAGGCTGACCTAGTATTGTTGAGTT 169
 QY 1505 TGGGGTTCCAGTACATGATGATGCTGCTGAGGAGCCCAATTTACATCCACCA 1564
 Db 168 TGGGGTTCCAGTACATGATGATGCTGCTGAGGAGCCCAATTTACATCCACCA 109
 QY 1565 TTACACAGCCCAACCCACCAAGGTGAAACCAACC 1599
 Db 108 TTACACAGCCCAACCCACCAAGGTGAAACCAACC 74
 RESULT 11
 LOCUS AL844326/c 599 bp mRNA linear EST 30-JUL-2002
 DEFINITION AL844326 pool_YT_11b_v_SPD Homo sapiens cDNA, mRNA sequence.
 ACCESSION AL844326
 VERSION AL844326.1 GI:22019106
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 599)
 Ashcroft, K., Bethel, G., Bye, J.M., Howell, G.R., Huckle, E.J. and
 Sheridan, E.
 Homo sapiens EST sequence
 Unpublished (2002)
 Contact: The Sanger Centre
 The Sanger Centre
 Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK
 Email: humquery@sanger.ac.uk
 Sanger Centre name : sccid10827.d1
 Homo sapiens EST sequence. This sequence was generated as part of
 The Wellcome Trust Sanger Institute program to identify and
 annotate genes in the human genome. Incomplete or unconfirmed genes
 are experimentally analysed using a variety of cDNA library
 resources. This sequence was obtained from a PCR product generated
 from a pool of up to 100,000 cDNA clones derived from
 pool_YT_11b_v_SPD cDNA library. Further information can be found at
 http://www.sanger.ac.uk/Teams/teams69/.
 Location/Qualifiers
 1. 599
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /map="20"
 /clone_lib="pool_YT_11b_v_SPD"
 /note="Organ: breast; Vector: pZERO-1; Site: 1; SphI;
 Site_2: SphI; Ductal carcinoma in situ, high-grade, comedo
 , from 41 yo female. Library constructed in the laboratory
 of K. Polyak, M.D., Ph.D. (Dana-Farber Cancer Institute)."
 BASE COUNT 142 a 148 c 165 g 144 t
 ORIGIN
 Query Match 20.0% Score 513; DB 9; Length 599;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 513; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1994 TAATTTTGTATTTTGTAGTACATGAGGTTTCCACCAATTGGCCAGGCTGTGCA 2053
 Db 520 TAATTTTGTATTTTGTAGTACATGAGGTTTCCACCAATTGGCCAGGCTGTGCA 461
 QY 2054 ACTCTGACCTCAGGATCCACCACTTGGCTCCCAAGTCTGGATTCAGAGGT 2113
 Db 460 ACTCTGACCTCAGGATCCACCACTTGGCTCCCAAGTCTGGATTCAGAGGT 401
 QY 2114 GAGCCAGGACCAACCTAGCTCAGATCTATTTATTTTGTGCTTACATTTCC 2173
 Db 400 GAGCCAGGACCAACCTAGCTCAGATCTATTTATTTTGTGCTTACATTTCC 341

QY 2174 TAGCAGCTGGGCTTGGCCATCTTGTGGCCGATATAAATAACCTTTAAGTCTAGCA 2233
 DB 340 TAGCAGCTGGGCTTGGCCATCTTGTGGCCGATATAAATAAATTAACCTTTAAGTCTAGCA 281
 QY 2234 CACTGACGTAGGCGCAGGACCTCAGTGTCTGGGCGGGGACCTCAGAAAGGTGCTAAGGCTT 2293
 DB 280 CACTGACGTAGGCGCAGGACCTCAGTGTCTGGGCGGGGACCTCAGAAAGGTGCTAAGGCTT 221
 QY 2294 CTCTCCCAATGCGCAAGACGAGACCAACAGCTTACCAACAAATCCAGGCTTGAATTTCCCT 2353
 DB 220 CTCTCCCAATGCGCAAGACGAGACCAACAGCTTACCAACAAATCCAGGCTTGAATTTCCCT 161
 QY 2354 GCTGCTCCATTAACGAAAGAGGTCTGTGTGATCCGCTAAGGAGATCAGGAGAGAGAA 2413
 DB 160 GCTGCTCCATTAACGAAAGAGGTCTGTGTGATCCGCTAAGGAGATCAGGAGAGAGAA 101
 QY 2414 AAGAGGATGGGGTGGAGAGCAACCCCTCCAGTCTCTTCTTCCCAAGCTACAGT 2473
 DB 100 AAGAGGATGGGGTGGAGAGCAACCCCTCCAGTCTCTTCTTCCCAAGCTACAGT 41
 QY 2474 GGGGTGGAAAGGCTTTATCAGGTATCATCAAC 2506
 DB 40 GGGGTGGAAAGGCTTTATCAGGTATCATCAAC 8

RESULT 12
 BG284179 566 bp mRNA linear EST 21-FEB-2001
 LOCUS 602408226F1 NIH_MGC_91 Homo sapiens cDNA clone IMAGE:4520382 5'
 DEFINITION mRNA sequence.
 ACCESSION BG284179
 VERSION BG284179.1 GI:13034866
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 566)
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strauberg, Ph.D.
 Email: cgapba-remail.nih.gov
 Tissue Procurement: DCTD/DTF
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: LLM10418 row: c column: 07
 High quality sequence start: 2
 High quality sequence stop: 566.

FEATURES

source
 1..566
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_image="4520382"
 /clone_id="NIH_MGC_91"
 /tissue_type="adenocarcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: prostate; Vector: PCMV-SPORT6; Site 1: NotI;
 Site 2: SalI; Cloned unidirectionally; oligo-dt primed.
 Average insert size 1.4 kb. Library enriched for
 full-length clones and constructed by Life Technologies.
 Note: this is a NIH_MGC library."
 BASE COUNT 116 a 187 c 152 g 110 t 1 others
 ORIGIN

Query Match 19.0%; Score 488; DB 12; Length 566;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 488; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 796 GGCCTTTACTCTGTGTGATCCGCTCAGCCGCTGATCTGGAGACGAGACAGAC 855
 DB 13 GGCCTTTACTCTGTGTGATCCGCTCAGCCGCTGATCTGGAGACGAGACAGAC 72
 QY 856 TACAGATCAATGCTCTTGAACAATGGCTGGCTGATCAATCAACCGGCTCACTTTCCC 915
 DB 73 TACAGATCAATGCTCTTGAACAATGGCTGGCTGATCAATCAACCGGCTCACTTTCCC 132
 QY 916 TCACTCAGGCGCTTGTGACCAATTAATCTGAGCTGGAGATGATCATCTGCTTACTC 975
 DB 133 TCACTCAGGCGCTTGTGACCAATTAATCTGAGCTGGAGATGATCATCTGCTTACTC 192
 QY 976 AAGAGCCCTGTGTCTGTGACAGAGGCTGGCCCTGCTGGCAAGATATACCTTACT 1035
 DB 193 AAGAGCCCTGTGTCTGTGACAGAGGCTGGCCCTGCTGGCAAGATATACCTTACT 252
 QY 1036 GTGACTGTGACAGAGACACCACTCACTGGAAGAGCTGACAGCTCCCTCTGTTTCT 1095
 DB 253 GTGACTGTGACAGAGACACCACTCACTGGAAGAGCTGACAGCTCCCTCTGTTTCT 312
 QY 1096 GAAGCTGCCACAGGGGAGAGCTCTTCTCAGTGAAGGCTCCGGGAGTCCCTAGCTTC 1155
 DB 313 GAAGCTGCCACAGGGGAGAGCTCTTCTCAGTGAAGGCTCCGGGAGTCCCTAGCTTC 372
 QY 1156 TACATCAGCTGAATGACGAGGCTGTCTTTGGATGATCCTTGAAGCCCAAGAGAGGC 1215
 DB 373 TACATCAGCTGAATGACGAGGCTGTCTTTGGATGATCCTTGAAGCCCAAGAGAGGC 432
 QY 1216 CAAAGAGGAAACCAAGGCTGACACCTTGAAGCCCAATTTAGCTTCTGGGACACCCAGA 1275
 DB 433 CAAAGAGGAAACCAAGGCTGACACCTTGAAGCCCAATTTAGCTTCTGGGACACCCAGA 492
 QY 1276 GGCAGAGC 1283
 DB 493 GGCAGAGC 500

RESULT 13
 AL844311 597 bp mRNA linear EST 30-JUL-2002
 LOCUS AL844311 pool_YT_11b_v_SPD Homo sapiens cDNA, mRNA sequence.
 ACCESSION AL844311
 VERSION AL844311.1 GI:22019093
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE 1 (bases 1 to 597)
 AUTHORS Ashcroft, K., Bethel, G., Bye, J.M., Howell, G.R., Huckle, E.J. and
 Sheridan, E.
 TITLE Homo sapiens EST sequence
 JOURNAL Unpublished (2002)
 COMMENT Contact: The Sanger Centre
 The Sanger Centre
 Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK
 Email: humquery@sanger.ac.uk
 Sanger Centre name: sccid0818.154136A
 Homo sapiens EST sequence. This sequence was generated as part of
 The Wellcome Trust Sanger Institute program to identify and
 annotate genes in the human genome. Incomplete or unconfirmed genes
 are experimentally analysed using a variety of cDNA library
 resources. This sequence was obtained from a PCR product generated
 from a pool of up to 100,000 cDNA clones derived from
 pool_YT_11b_v_SPD cDNA library. Further information can be found at
 http://www.sanger.ac.uk/Teams/Team9/.

FEATURES

source
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 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /map="20"
 /clone_id="pool_YT_11b_v_SPD"
 /note="Organ: breast; Vector: pZERO-1; Site 1: SpH1;
 Location/Qualifiers


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/clone_lib="NCI_CGAP_Lym12"
/issue_type="lymphoma, follicular mixed small and large
cell"
/lab_host="DH10B"
/note="Organ: lymph node; Vector: pCMV-Sport6; Site: 1;
Sal: Site 2: Not; Cloned unidirectionally. Primer:
Oligo dt. Average insert size 1.25 kb. Life Technologies
catalog #: 11547-015"

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BASE COUNT      94 a      100 c      109 g      106 t
ORIGIN

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Query Match      15.9%; Score 409; DB 9; Length 409;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 2127 CAGCTAGCTCTCAGATCTCTATTTCAATTTTGTGCTTACCAATCCCTACACACTGGCC 2186
DB 409 CAGCTAGCTCTCAGATCTCTATTTCAATTTTGTGCTTACCAATCCCTACACACTGGCC 350
QY 2187 TTGCATCTTTGTGCGCAATTAATAATACACCTCTTAAGTCTAGACACTGAGTGAAG 2246
DB 349 TTGCATCTTTGTGCGCAATTAATAATAATACACCTCTTAAGTCTAGACACTGAGTGAAG 290
QY 2247 CCAGGACACTCAGTGTGGGCGAGGGGATAGAAAGGTGCTTAAGCCCTCTCCACAAATGC 2306
DB 289 CCAGGACACTCAGTGTGGGCGAGGGGATAGAAAGGTGCTTAAGCCCTCTCCACAAATGC 230
QY 2307 CAAGCGAGACCAACAGCTTAACCAATCAGCCCTTGAATTTCCCTGCTGCTCCATTA 2366
DB 239 CAAGCGAGACCAACAGCTTAACCAATCAGCCCTTGAATTTCCCTGCTGCTCCATTA 170
QY 2367 ACAGAAAGAGTCTGTGGATCCGCTAAGGATCAGGGAGGAGAAAGAGGATGGGG 2426
DB 169 ACAGAAAGAGTCTGTGGATCCGCTAAGGATCAGGGAGGAGAAAGAGGATGGGG 110
QY 2427 TGGAGGCAACCCCTCTCAGTGTCTTAAGTCCCAAGCTACAGTGGGGTGGAAAAG 2486
DB 109 TGGAGGCAACCCCTCTCAGTGTCTTAAGTCCCAAGCTACAGTGGGGTGGAAAAG 50
QY 2487 CTTATCAGGTATCATCAACAGGTTCTCAATTAAGATTATTTATTC 2535
DB 49 CTTATCAGGTATCATCAACAGGTTCTCAATTAAGATTATTTATTC 1

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RESULT 19
BF057252/c      397 bp      mRNA      linear      EST 16-OCT-2000
LOCUS      7k18a03.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:3444389 3',
DEFINITION      mRNA sequence.
ACCESSION      BF057252
VERSION      BF057252.1 GI:10811148
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

```

```

REFERENCE
AUTHORS      1 (bases 1 to 397)
TITLE      NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
JOURNAL      National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
COMMENT      Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL, send email to:
info@image.lnl.gov
Seq primer: -40UP from Gibco.

```

FEATURES

source

```

Location/Qualifiers
1..397
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="IMAGE:3444389"
/clone_lib="NCI_CGAP_GC6"
/issue_type="pooled germ cell tumors"
/lab_host="DH10B"
/note="Vector: pRTT3D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not 1; Site 2: Eco RI; Plasmid DNA
from the normalized library NCI CGAP GC4 was prepared, and
ss circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (cloneids
1257096-1258631, 1467064-1470983, and 1475592-1476743).
Subtraction by Bento Soares and M. Fatima Bonaldo. "

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BASE COUNT

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88 a      100 c      109 g      109 t
ORIGIN

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Query Match      15.5%; Score 397; DB 12; Length 397;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 397; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 2154 TTTTGTGCTTACCAATTCCTAGACACTGCGCTTGCATCTTTGTGCGCAATTAATAAT 2213
DB 397 TTTTGTGCTTACCAATTCCTAGACACTGCGCTTGCATCTTTGTGCGCAATTAATAAT 338
QY 2214 AACACCTCTTAAGTCTAGACACTGCGCTTGCATCTTTGTGCGCAATTAATAAT 2273
DB 337 AACACCTCTTAAGTCTAGACACTGCGCTTGCATCTTTGTGCGCAATTAATAAT 278
QY 2274 ATCAGAGGTGCTTAAGCCCTCTCTCCAAATGCCAAGCGAGACCAACAGCTTAACCAA 2333
DB 277 ATCAGAGGTGCTTAAGCCCTCTCTCCAAATGCCAAGCGAGACCAACAGCTTAACCAA 218
QY 2334 ATCCAGCCCTTGAATTTCCCTGCTGCTCCATTAACAGAAAGAGTGTGGATCCGCTA 2293
DB 217 ATCCAGCCCTTGAATTTCCCTGCTGCTCCATTAACAGAAAGAGTGTGGATCCGCTA 158
QY 2394 AGGATTCAGGAGAGAGAAAGAGGATGGGGTGGAGGACCCCTCTCAAGTCTCTTA 2453
DB 157 AGGATTCAGGAGAGAGAAAGAGGATGGGGTGGAGGACCCCTCTCAAGTCTCTTA 98
QY 2454 CTGGTTCCTCAAGCTACAGTGTGGGAGGAGGCTTATCAGGTATCATCAACAGTTCT 2513
DB 97 CTGGTTCCTCAAGCTACAGTGTGGGAGGAGGCTTATCAGGTATCATCAACAGTTCT 38
QY 2514 CAATTAAAGTTGATTTTATTCAGTATGTGAAAAA 2550
DB 37 CAATTAAAGTTGATTTTATTCAGTATGTGAAAAA 1

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RESULT 20
BF062179/c      397 bp      mRNA      linear      EST 16-OCT-2000
LOCUS      7k73e03.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:3481060 3',
DEFINITION      mRNA sequence.
ACCESSION      BF062179
VERSION      BF062179.1 GI:10821089
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

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REFERENCE
AUTHORS      1 (bases 1 to 397)
TITLE      NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
JOURNAL      National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
COMMENT      Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael

```

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CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL, send email to:
info@image.lnl.gov
Seq primer: -40UP from Gibco.

```


DEFINITION	7k65h11.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:3480452 3', mRNA sequence.
ACCESSION	BF059756
VERSION	BF059756.1
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
AUTHORS	1 (bases 1 to 397)
TITLE	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .
JOURNAL	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
COMMENT	Unpublished (1997) Contact: Robert Strausberg, Ph.D. Email: cga06@lewell.nhl.gov Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL, send email to: infoimage.llnl.gov Seq primer: -400p from Glibco.
FEATURES	Location/Qualifiers
source	<pre>1..397 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:3480452" /clone_1lb="NCI CGAP GC6" /tissue_type="pooled germ cell tumors" /lab_host="DH10B" /notes="Vector: p773D-Pac (Pharmacia) with a modified polyLinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA from the normalized library NCI CGAP GC4 was prepared, and 58 circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clonids 1257096-1258631, 1469064-1470983, and 1475592-1476743). Subtraction by Bento Soares and M. Fatima Bonaldo."</pre>
BASE COUNT	89 a 99 c 99 g 110 t
ORIGIN	
Query Match	11.5%; Score 295; DB 12; Length 397;
Best Local Similarity	99.5%; Pred. No. 0;
Matches 395; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
2154	TTTGTGCTTACCATTCCTGTACACACTGGGCGCTCCATCTGTGGCGCAATATTAAT 2213
397	TTTGTGGCTTACCATTCCTGTACACACTGGGCGCTCCATCTGTGGCGCAATATTAAT 338
2214	AACACCTTTAAGTTAGTACACACTGCAATGAGCCACGACCTCAAGTCTGGCAGGGGC 2273
337	AACACCTTTAAGTTAGTACACACTGCAATGAGCCACGACCTCAAGTCTGGCAGGGGC 278
2274	ATCAGAAGTGCTTAAGCCCTCTCTCCAAATGCGAAGCGAGACACAGCTTACACAA 2333
277	ATCAGAAGTGCTTAAGCCCTCTCTCCAAATGCGAAGCGAGACACAGCTTACACAA 218
2334	ATTCAGCGCTTATTTCCCTGCGGCTCCATTAACGAAAGAGGTGCTGGATCCGCTA 2393
217	ATTCAGCGCTTATTTCCCTGCGGCTCCATTAACGAAAGAGGTGCTGGATCCGCTA 158
2394	AGGATATGAGGAGAGAAAGAAAGAGATGGGGTGGAGAGCAACCCCTCAAGTCTCTTA 2453
157	AGGATATGAGGAGAGAAAGAAAGAGATGGGGTGGAGAGCAACCCCTCAAGTCTCTTA 98
2454	CTGGATCCCAACTACAGTGGGGTGGAGAGGCTTATCAGATATCATCAACAGTTCT 2513
97	CTGGATCCCAACTACAGTGGGGTGGAGAGGCTTATCAGATATCATCAACAGTTCT 38

The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208

FEATURES
SOURCE

```

Location/Qualifiers
1. .489
/organism="Homo sapiens"
/db_xref="GDB:7542514"
/db_xref="EAXON:9606"
/clone="RPC1-11-111L1"
/clone_lib="RPC1-11"
/clone_lib="RPC1-11"
/sex="Male"
/cell_type="Lymphocytes"
/notes="vector: pBAc3 6; Site_1: EcoRI; Site_2: EcoRI
Rep11 Human Male BAC library"
140 a 100 c 102 g 147 t

```

Qy 2035 TTGGCCAGGCTGTGTCTGAACTCTGACCTCAGGTATCCACCCACTTTGGCCTCCCAA 2094
Dp 372 TTGGCCAGGCTGTGTCTGAACTCTGACCTCAGGTATCCACCCACTTTGGCCTCCCAA 313

RESULT 31

LOCUS	AQ431946	534 bp	DNA	linear	GSS 31-MAR-1999
DEFINITION	HS_5065_A2_F08_T7A RPT-11 Human Male BAC Library Homo sapiens genomic clone Plate=641 Col=16 Row=K, DNA sequence.				
ACCESSION	U00310.6				

TITLE	Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
MEDLINE	99380589
COMMENT	Contact: Mahairas GG, Wallace JC, Hood L

```

Plate: 641 row: K column: 16
Seq primer: T7
Class: BAC ends
High quality sequence stop: 534
location/Qualifiers
1..534
FEATURES
source
```

Oy	2095	GTGCTGGGATTACA	2108
Db	341	GTGCTGGGATTACA	328

0
1
2
3
4
5

ACCESSION	BC943350
VERSION	BC943350.1
KEYWORDS	EST,
SOURCE	human.

FEATURES

SOURCE

```

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="ax35b11"
/clone_lib="Proliferating Human Erythroid Cells (LCB:ax
library)"
/sex="unknown"
/tissue_type="blood"
/cell_type="Erythroid Cells"
/cell_line="Primary Culture of Peripheral Blood
Mononuclear Cells"

```

```

/dev stage="Progenitor; EPO responsive CD11a+++"
/lab host="SOLR"
/note="Organ: Blood; Vector: Lambda ZAP II; Site 1: EcoRI;
Site 2: EcoRI; 65,000 proliferating erythroid cells from
the buffy coat of a blood donation were obtained by flow
cytometric separation after a 5-day culture period in the
presence of erythropoietin. Total RNA was purified from
the sorted cell population using TRIzol reagent. RNA (0.3
ug) was converted into double stranded cDNA using
Clontech's Capfinder cDNA Library Construction Kit
(Clontech) according to the manufacturer's protocol and
cloned into EcoRI digested Lambda Zap II vector
(Stratagene). The phage library was amplified once prior
to in vivo excision in SOLR cells. Individual colonies
were grown, and the cDNA inserts were sequenced in high
throughput (NIH intramural sequencing center
http://www.nhgsc.nih.gov/)."
BASE COUNT      162 a      122 c      144 g      144 t
ORIGIN
Query Match      2.8%; Score 73; DB 13; Length 572;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2050 TCGAATCTCGAGTGTATCCACCCACCTGGCCCAAGTCTGGATTACAG 2109
DB 375 TCGAATCTCGAGTGTATCCACCCACCTGGCCCAAGTCTGGATTACAG 316

QY 2110 GTGTGAGCCACG 2122
DB 315 GTGTGAGCCACG 303

RESULT 33
AM247089      503 bp      mRNA      linear      EST 07-JAN-2000
LOCUS      2822458.Sprime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822458 5',
DEFINITION      mRNA sequence.
ACCESSION      AM247089
VERSION      AM247089.1 GI:6590082
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE      1 (bases 1 to 503)
AUTHORS      NIH-MGC http://www.ncbi.nlm.nih.gov/.
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      Other ESTs: 2822458.Sprime
Contact: Robert Strausberg, Ph.D.
Email: cga@dbi-remail.nih.gov
Tissue Procurement: DCTD/DRP cDNA Library Preparation: Ling
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
Consortium (ILNI) DNA Sequencing by: Berkeley MGC sequencing
project Clone distribution: MGC clone distribution information can
be found through the I.M.A.G.E. Consortium/ILNI at:
www.bio.lnlnl.gov/bdrrp/image/image.html Base Calling / Quality
Trimming: cross match from University of Washington Genome Center
PhRAP suite. Poly-T identification: patmatch.pl from Berkeley
Drosophila Genome Project. University of Washington Genome Center:
http://www.genome.washington.edu
Plate: L1CM9 row: H column: 11
High quality sequence stop: 454.
Location/Qualifiers
1..503
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2822458"
/clone_1ib="NIH_MGC_7"
/tissue type="small cell carcinoma"
/cell_line="MGC3"

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/lab host="DH10B (phage-resistant)"
/note="Organ: lung; Vector: pOTR1; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adapter: GGCAAGAG(G). Site selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
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```

BASE COUNT      110 a      149 c      117 g      127 t
ORIGIN
Query Match      2.8%; Score 71; DB 10; Length 503;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2050 TCGAATCTCGAGTGTATCCACCCACCTGGCCCAAGTCTGGATTACAG 2109
DB 199 TCGAATCTCGAGTGTATCCACCCACCTGGCCCAAGTCTGGATTACAG 258

QY 2110 GTGTGAGCCAC 2120
DB 259 GTGTGAGCCAC 269

RESULT 34
BQ016908      637 bp      mRNA      linear      EST 17-JUN-2002
LOCUS      UT-H-D10-auz-d-06-0-UT.s1 NCI CGAP_D10 Homo sapiens cDNA clone
DEFINITION      IMAGE:5876309 3', mRNA sequence.
ACCESSION      BQ016908
VERSION      BQ016908.1 GI:19752185
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE      1 (bases 1 to 637)
AUTHORS      NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE      National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
JOURNAL      Tumor Gene Index
COMMENT      Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cga@dbi-remail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be found
through the I.M.A.G.E. Consortium/ILNI at: http://image.lnlnl.gov
The following repetitive elements were found in this cDNA
Sequence: 14-143->Alu (matched complement)
Seq primer: M13 FORWARD
POLYA=yes.
Location/Qualifiers
1..637
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5876309"
/clone_1ib="NCI_CGAP_D10"
/tissue type="NCI_CGAP_D10"
/dev stage="Adult"
/lab host="DH10B (Life Technologies)"
/note="Organ: lung; Vector: pRTT3-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;
NCI CGAP D10 is a cDNA library containing the following
tissue(s): A pool of lung Focal Fibrosis. The library was
constructed according to Bonaldi, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cDNA was ligated to an EcoR I
adapter, digested with Not I, and cloned directionally
into pRTT3-Pac vector. The oligonucleotide used to prime

```

the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dtt)18 tail. The sequence tag for this library is ATACCGCGTC.

TAG_LIB=UI-H-D10
TAG_TISSUE=lung with fibrosis
TAG_SEQ=ATACCGCGTC

BASE COUNT 148 a 149 c 165 g 174 t 1 others
ORIGIN

Query Match 2.8%; Score 71; DB 14; Length 637;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2050 TCGAAGCTCTGAGCTGATGATCCACCCAGCTTGGCTCCCAAGTGTGGGATTACAG 2109
Db 62 TCGAAGCTCTGAGCTGATGATCCACCCAGCTTGGCTCCCAAGTGTGGGATTACAG 121
Qy 2110 GTGTGAGCCAC 2120
Db 122 GTGTGAGCCAC 132

RESULT 35
BM997767 671 bp mRNA linear EST 17-JUN-2002
LOCUS UI-H-D10-aw-1-02-0-UI.s1 NCI_CGAP_D10 Homo sapiens cDNA clone
DEFINITION IMAGE:5875273 3', mRNA sequence.
ACCESSION BM997767
VERSION BM997767.1 GI:19722668
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 671)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strauberg, Ph.D.
Email: cga@nci.nih.gov
Tissue Procurement: Dr. Jose Mercuende
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be found
through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov
The following repetitive elements were found in this cDNA
sequence: 8-235, >Alu (matched complement)
Seq primer: M13 FORWARD
POLYA=788.

FEATURES
Location/Qualifiers

1..671
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5875273"
/clone_lib="NCI CGAP D10"
/tissue_type="lung Focal Fibrosis"
/dev_stage="Adult"

/lab_host="DH10B (Life Technologies)"
/note="Organ: Lung; Vector: p773-Pac (Pharmacia) with a
modified polylinker; Site 1: Ecor I; Site 2: Not I;
NCI CGAP D10 is a cDNA library containing the following
tissue(s): A pool of lung focal fibrosis. The library was
constructed according to Bonaldi, Lemmon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cDNA was ligated to an Ecor I
adaptor, digested with Not I, and cloned directionally
into p773-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the

(dtt)18 tail. The sequence tag for this library is ATACCGCGTC.

TAG_LIB=UI-H-D10
TAG_TISSUE=lung with fibrosis
TAG_SEQ=ATACCGCGTC

BASE COUNT 149 a 173 c 167 g 180 t 2 others
ORIGIN

Query Match 2.8%; Score 71; DB 14; Length 671;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2050 TCGAAGCTCTGAGCTGATGATCCACCCAGCTTGGCTCCCAAGTGTGGGATTACAG 2109
Db 214 TCGAAGCTCTGAGCTGATGATCCACCCAGCTTGGCTCCCAAGTGTGGGATTACAG 273
Qy 2110 GTGTGAGCCAC 2120
Db 274 GTGTGAGCCAC 284

RESULT 36
AG010953 700 bp DNA linear GSS 14-APR-1999
LOCUS AG010953
DEFINITION Homo sapiens genomic DNA, 21q region, clone: S594BG38, genomic
survey sequence.
ACCESSION AG010953 AG004614
VERSION AG010953.1 GI:3347781
KEYWORDS GSS.
SOURCE Homo sapiens DNA, clone: S594BG38.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 700)
AUTHORS Hattori, M., Ishii, K., Toyoda, A., Shiba, T. and Sakaki, Y.
TITLE Homo sapiens genomic DNA, chromosome 21q
REFERENCE 2 (bases 1 to 700)
AUTHORS Hattori, M., Ishii, K., Toyoda, A., Shiba, T. and Sakaki, Y.
TITLE Direct Submission
JOURNAL Submitted (28-JUL-1998) Masahira Hattori, Kitasato University,
Department of Science, JST Sequencing Laboratory, Kitasato 1-15-1,
Sagamihara 428, Japan (E-mail: hattori@hgc.jst.go.jp)
Tel: 0427-78-9732, Fax: 0427-78-9561
On Feb 5, 1999 this sequence version replaced gi:2822077.
AG004614: Submitted (29-Jan-1998).

COMMENT
Location/Qualifiers

1..700
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="21"
/map="21q"
/clone="S594BG38"

BASE COUNT 149 a 161 c 178 g 143 t 69 others
ORIGIN

Query Match 2.8%; Score 71; DB 17; Length 700;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2050 TCGAAGCTCTGAGCTGATGATCCACCCAGCTTGGCTCCCAAGTGTGGGATTACAG 2109
Db 335 TCGAAGCTCTGAGCTGATGATCCACCCAGCTTGGCTCCCAAGTGTGGGATTACAG 276
Qy 2110 GTGTGAGCCAC 2120
Db 275 GTGTGAGCCAC 265

RESULT 37
BS904397 737 bp mRNA linear EST 20-OCT-2000
LOCUS BS904397
DEFINITION 60149631371 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3898443 5',

mRNA sequence.
 BE904397
 BE904397.1 GI:10396608
 EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 1 (bases 1 to 737)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 CONTACT: Robert Strausberg, Ph.D.
 Email: cgaabs-r@mail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLM9694 row: i column: 04
 High quality sequence stop: 673.
 Location/Qualifiers
 1..737
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_image="3898443"
 /clone_lib="NIH_MGC_48"
 /tissue_type="epithelioid carcinoma"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: pancreas; Vector: pCMV-SPORT6; Site 1: NotI;
 Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
 Average insert size 1.1 Kb. Library constructed by Life
 Technologies."
 BASE COUNT 162 a 187 c 196 g 192 t
 ORIGIN
 Query Match 2.8%; Score 71; DB 12; Length 737;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2050 TCGAAGCTCTGAGCTGATCCACCCAGCTTGGCTCCCAAGTCTGGATTACAG 2109
 |||||
 DB 216 TCGAAGCTCTGAGCTGATCCACCCAGCTTGGCTCCCAAGTCTGGATTACAG 275
 |||||
 QY 2110 GTGTAGCCAC 2120
 |||||
 DB 276 GTGTAGCCAC 286
 |||||
 RESULT 38
 BF664472 832 bp mRNA linear EST 21-DEC-2000
 LOCUS 602146224F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4309876 5',
 DEFINITION mRNA sequence.
 ACCESSION BF664472
 VERSION BF664472.1 GI:11938277
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 1 (bases 1 to 832)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 CONTACT: Robert Strausberg, Ph.D.
 Email: cgaabs-r@mail.nih.gov
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 CDNA Library Preparation: Ling Hong/Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLM1183 row: p column: 05
 High quality sequence stop: 679.
 Location/Qualifiers
 1..832
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_image="4309876"
 /clone_lib="NIH_MGC_48"
 /tissue_type="primary B-cells from tonsils (cell line)"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: B-cells; Vector: pOT87; Site 1: XhoI;
 Site 2: EcoRI; CDNA made by oligo-dt priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGCAGAG(G). Size-selected >500bp
 for average insert size 1.8kb. Library constructed by Ling
 Hong in the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC Library."
 BASE COUNT 168 a 221 c 228 g 215 t
 ORIGIN
 Query Match 2.8%; Score 71; DB 12; Length 832;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2050 TCGAAGCTCTGAGCTGATCCACCCAGCTTGGCTCCCAAGTCTGGATTACAG 2109
 |||||
 DB 253 TCGAAGCTCTGAGCTGATCCACCCAGCTTGGCTCCCAAGTCTGGATTACAG 312
 |||||
 QY 2110 GTGTAGCCAC 2120
 |||||
 DB 313 GTGTAGCCAC 323
 |||||
 RESULT 39
 BG758454 896 bp mRNA linear EST 15-MAY-2001
 LOCUS 602712653F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4853076 5',
 DEFINITION mRNA sequence.
 ACCESSION BG758454
 VERSION BG758454.1 GI:14069107
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 1 (bases 1 to 896)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 CONTACT: Robert Strausberg, Ph.D.
 Email: cgaabs-r@mail.nih.gov
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 CDNA Library Preparation: Ling Hong/Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLM1698 row: i column: 13
 High quality sequence stop: 733.
 Location/Qualifiers
 1..896
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_image="4853076"
 /clone_lib="NIH_MGC_48"
 /tissue_type="primary B-cells from tonsils (cell line)"
 /lab_host="DH10B (phage-resistant)"

/note="Organ: B-cells; Vector: pOT87; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC library."

BASE COUNT 206 a 219 c 240 g 231 t
ORIGIN

Query Match 2.8%; Score 71; DB 12; Length 896;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2050 TCGAAGCTCTGACCTGAGTATGATCCACCCAGCTGGCCCAAGGCTGGGATTACAGT 2109
DB 257 TCGAAGCTCTGACCTGAGTATGATCCACCCAGCTGGCCCAAGGCTGGGATTACAGT 316

QY 2110 GTGTAGCCAC 2120
DB 317 GTGTAGCCAC 327

RESULT 40
LOCUS A0261419 581 bp DNA linear GSS 24-OCT-1998
DEFINITION CITR1-E1-2509P17.TF CITR1-E1 Homo sapiens genomic clone 2509P17,
A0261419
DNA sequence.
A0261419
GSS.
A0261419.1 GI:3787943
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 581)
Adams, M.D., Rounsley, S.D., Zhao, S., Baas, S., Linher, K., Golden, K.,
Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and
Venter, J.C.
Use of a random human BAC End Sequence Database for Sequence-Ready
Map Building
Unpublished (1998)
Other_GSSs: CITR1-E1-2509P17.TF
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdamas@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/hungen/bac_end_search/bac_end_search.html.
Seq primer: M13-21
Class: BAC ends.

TITLE Map Building
JOURNAL Unpublished (1998)
COMMENT Other_GSSs: CITR1-E1-2509P17.TF

FEATURES
source location/Qualifiers
1..581
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="2509P17"
/clone_1db="CITR1-E1"
/sex="male"
/cell_type="sperm"
/note="Vector: pBeloBAC11; Site_1: EcoRI; Site_2: EcoRI;
Caltech Human BAC Library D"
BASE COUNT 180 a 131 c 151 g 119 t
ORIGIN

Query Match 2.7%; Score 69; DB 17; Length 581;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2052 GAAGTCTGACCTGAGTATGATCCACCCAGCTTGGCTCCCAAGTCTGGGATTACAGT 2111
DB 511 GAAGTCTGACCTGAGTATGATCCACCCAGCTTGGCTCCCAAGTCTGGGATTACAGT 452
QY 2112 GTGAGCCAC 2120
DB 451 GTGAGCCAC 443

RESULT 41
LOCUS A0542542 596 bp DNA linear GSS 19-MAY-1999
DEFINITION RPCI-11-347J18.TV RPCI-11 Homo sapiens genomic clone RPCI-11-347J18
A0542542
DNA sequence.
A0542542
GSS.
A0542542.1 GI:4872998
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 596)
Zhao, S., Adams, M.D., Niernan, W., Malek, J., de Jong, P. and Venter
J.C.
Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
Map Building
Unpublished (1997)
Other_GSSs: RPCI-11-347J18.TV
Contact: Shaying Zhao, William Niernan, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbe@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pdejong@med.buffalo.edu). Clones may be purchased from
BACBAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genes (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/hungen/bac_end_search/bac_end_search.html.
Seq primer: T7
Class: BAC ends.

FEATURES
source location/Qualifiers
1..596
/organism="Homo sapiens"
/db_xref="GDB:7633097"
/db_xref="taxon:9606"
/clone="RPCI-11-347J18"
/clone_1db="RPCI-11"
/sex="Male"
/cell_type="Lymphocytes"
/note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCI11 Human Male BAC Library"
BASE COUNT 145 a 143 c 109 g 198 t 1 others
ORIGIN

Query Match 2.7%; Score 69; DB 17; Length 596;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2052 GAAGTCTGACCTGAGTATGATCCACCCAGCTTGGCTCCCAAGTCTGGGATTACAGT 2111
DB 503 GAAGTCTGACCTGAGTATGATCCACCCAGCTTGGCTCCCAAGTCTGGGATTACAGT 562
QY 2112 GTGAGCCAC 2120
DB 563 GTGAGCCAC 571

RESULT 42
A0348722/c

LOCUS AQ348722 617 bp DNA linear GSS 07-MAY-1999
 DEFINITION RPEC11-11617.TU RPEC1-11 Homo sapiens genomic clone RPEC1-11-11617,
 DNA sequence.
 ACCESSION AQ348722
 VERSION AQ348722.1 GI:4173618
 KEYWORDS GSS.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 617)
 AUTHORS Zhao, S., Adams, M.D., Nierman, W., Malek, J., de Jong, P. and Venter,
 J.C.
 TITLE Use of BAC End Sequences from Library RPEC1-11 for Sequence-Ready
 Map Building
 JOURNAL Unpublished (1997)
 COMMENT Other GSSs: RPEC11-11617.TU
 Contact: Shaying Zhao, William Nierman, Mark Adams
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850
 Tel: 301 838 0208
 Fax: 301 838 0208
 Email: hbe@tigr.org
 Clones are derived from the human BAC library RPEC1-11. For BAC
 library availability, please contact Pieter de Jong
 (peter@dejong.med.buffalo.edu). Clones may be purchased from
 BACPAC Resources (<http://bacpac.med.buffalo.edu/ordering/>) or from
 Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/cdb/humgen/bac_end_search/bac_end_search.html
 Seq primer: SP6
 Class: BAC ends.

FEATURES
 source
 1..617
 /organism="Homo sapiens"
 /db_xref="GDB:7544358"
 /db_xref="taxon:9606"
 /clone="RPEC1-11-11617"
 /clone_11b="RPEC1-11"
 /sex="Male"
 /cell_type="Lymphocytes"
 /note="Vector: pBAC3.5; Site 1: EcoRI; Site 2: EcoRI;
 RPEC11 Human Male BAC library"
 BASE COUNT 143 a 140 c 142 g 192 t
 ORIGIN

Query Match 2.7%; Score 69; DB 17; Length 617;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2052 GAATCTGAGCTGATTCACCCACCTTGCCCTCCCAAGTCTGGATTACAGGT 2111
 |||||||
 DB 291 GAATCTGAGCTGATTCACCCACCTTGCCCTCCCAAGTCTGGATTACAGGT 232
 |||||||

QY 2112 GTGAGCCAC 2120
 |||||||
 DB 231 GTGAGCCAC 223
 |||||||

RESULT 43
 AI902426/c 262 bp mRNA linear EST 30-MAR-2000
 LOCUS AI902426
 DEFINITION CM-BT006-080299-139 BT006 Homo sapiens cDNA, mRNA sequence.
 ACCESSION AI902426
 VERSION AI902426.1 GI:6492813
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 262)
 AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
 Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,

Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
 Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare,
 M.J., Soares, F., Brenatti, R.R., Reis, L.F., de Souza, S.J. and
 Simpson, A.J.
 Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 20202663
 CONTACT: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the PAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/seq/gethtml.pl?cl=CM&cl2=CM-BT006-139.html>)
 (ct3=080299&cl=1)
 Seq primer: pUC 18 forward.
 Location/Qualifiers
 1..262
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_11b="BT006"
 /sex="Female"
 /dev_stage="Adult"
 /note="Organ: breast; Vector: pUC18; Site 1: SmaI; Site 2:
 SmaI; A mini-library was made by cloning products derived
 from ORESTES PCR (U.S. Letters Patent application No. 196
 716 - Ludwig Institute for Cancer Research) profiles
 into the pUC 18 vector. Reverse transcription of tissue
 mRNA and cDNA amplification were performed under low
 stringency conditions."
 BASE COUNT 83 a 58 c 68 g 44 t 9 others
 ORIGIN

Query Match 2.6%; Score 68; DB 9; Length 262;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2053 AACTCTGAGCTGATTCACCCACCTTGCCCTCCCAAGTCTGGATTACAGGT 2112
 |||||||
 DB 193 AACTCTGAGCTGATTCACCCACCTTGCCCTCCCAAGTCTGGATTACAGGT 134
 |||||||

QY 2113 TGAGCCAC 2120
 |||||||
 DB 133 TGAGCCAC 126
 |||||||

RESULT 44
 BF753734/c 420 bp mRNA linear EST 10-JAN-2001
 LOCUS BF753734
 DEFINITION IL5-CT0521-031000-163-F02 CT0521 Homo sapiens cDNA, mRNA sequence.
 ACCESSION BF753734
 VERSION BF753734.1 GI:12080410
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 420)
 AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
 Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
 Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
 Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare,
 M.J., Soares, F., Brenatti, R.R., Reis, L.F., de Souza, S.J. and
 Simpson, A.J.
 Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 20202663

COMMENT

Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br

This sequence was derived from the PAPSP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=115&t=115-CT0521-
031000-163-f02&t3=2000-10-03&t4=1)
Seq primer: puc 18 forward

High quality sequence stop: 418.

FEATURES

Source

1. 420

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_id="CT0521"

/dev_stage="Adult"

/note="Organ: colon; Vector: puc18; Site_1: Sma1; Site_2:
Sma1; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No. 196
716 - Ludwig Institute for Cancer Research) profiles
into the puc 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."

BASE COUNT

127 a 86 c 113 g 94 t

ORIGIN

Query Match

Best Local Similarity 100.0%; Pred. No. 0;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2053 AACTCTGACCTGAGTATTCACCCACCTGCTCCCAAGTCTGGATTACAGGTG 2112
DB 243 AACTCTGACCTGAGTATTCACCCACCTGCTCCCAAGTCTGGATTACAGGTG 184
QY 2113 TGAGCCAC 2120
DB 183 TGAGCCAC 176

RESULT 45

A0583583

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

436 bp DNA linear GSS 07-JUN-1999
A0583583
RPCI-11-454D13.TV RPCI-11 Homo sapiens genomic clone RPCI-11-454D13
DNA sequence.
A0583583.1 GI:5010693
GSS.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 436)
Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter
J.C.
Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
Map Building
Unpublished (1997)
Other GSSs: RPCI-11-454D13.TV
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbeet@igir.org

Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from

Research Genet cs (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/hungen/bac_end_search/bac_end_search.html.
Seq primer: T7
Class: BAC ends.

FEATURES

Source

1. 436

/organism="Homo sapiens"

/db_xref="GDB:7674036"

/db_xref="taxon:9606"

/clone="RPCI-11-454D13"

/clone_id="RPCI-11"

/sex="Male"

/cell_type="Lymphocytes"

/note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCI11 Human Male BAC library"

BASE COUNT

75 a 148 c 91 g 121 t 1 others

ORIGIN

Query Match

Best Local Similarity 100.0%; Pred. No. 0;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2053 AACTCTGACCTGAGTATTCACCCACCTGCTCCCAAGTCTGGATTACAGGTG 2112
DB 83 AACTCTGACCTGAGTATTCACCCACCTGCTCCCAAGTCTGGATTACAGGTG 142
QY 2113 TGAGCCAC 2120
DB 143 TGAGCCAC 150

RESULT 46

A0462891

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

531 bp DNA linear GSS 23-APR-1999
A0462891
HS 5212 At B12.T7A RPCI-11 Human Male BAC library Homo sapiens
genomic clone Plate=788 Col=23 Row=C, DNA sequence.
A0462891.1 GI:4635661
GSS.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 531)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.
Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
99380589
Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu

Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering bac.htm)
or from Research Genetics (info@resgen.com). BAC end web server:
http://www.htec.washington.edu
Plate: 788 Row: C Column: 23
Seq primer: T7
Class: BAC ends
High quality sequence stop: 531.

FEATURES

Source

1. 531

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="Plate=788 Col=23 Row=C"

/clone_lib="RPCI-11 Human Male BAC library"
 /sex="male"
 /note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI;
 Male blood DNA was isolated from one randomly chosen donor
 and partially digested with a combination of EcoRI and
 EcoRI Methylase. Size selected DNA was cloned into the
 pBAC3.6 vector at EcoRI sites"

BASE COUNT 148 a 123 c 101 g 146 t 13 others
 ORIGIN
 Query Match 2.6%; Score 68; DB 17; Length 531;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2053 AACTCGTACCTGATGATCCACCCAGCTTGGCTCCCAAGTCTGGATTACAGGTG 2112
 |||||
 DB 432 AACTCGTACCTGATGATCCACCCAGCTTGGCTCCCAAGTCTGGATTACAGGTG 491
 |||||
 OY 2113 TGAGCCAC 2120
 |||||
 DB 492 TGAGCCAC 499

RESULT 47
 AOS56467 546 bp DNA linear GSS 29-MAY-1999
 LOCUS HS_5236_B1_C01.T7A RPCI-11 Human Male BAC Library Homo sapiens
 DEFINITION genomic clone Plate=812 Col=1 Row=F, DNA sequence.

ACCESSION AOS56467
 VERSION AOS56467.1 GI:4916199
 KEYWORDS GSS.

SOURCE human.
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 546)
 AUTHORS Mahaitas G.G., Wallace J.C., Smith K., Swartzell S., Holzman T.,
 Keller A., Shaker R., Furlong J., Young J., Zhao S., Adams M.D. and
 Hood L.

TITLE Sequence-tagged connectors: A sequence approach to mapping and
 scanning the human genome
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
 MEDLINE 99380589
 COMMENT Contact: Mahaitas GG, Wallace JC, Hood L
 High Throughput Sequencing Center
 University of Washington
 401 Queen Anne Avenue North, Seattle, WA 98109, USA
 Tel: (206) 616-3618
 Fax: (206) 616-3887
 Email: jwallace@u.washington.edu

Clones are derived from the human BAC library RPCI-11. For BAC
 library availability, please contact Pieter de Jong
 (pieter@dejong.med.buffalo.edu). Clones may be purchased from
 BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
 or from Research Genetics (info@resgen.com). BAC end Web Server:
 http://www.htsc.washington.edu
 Plate: 812 row: F column: 1
 Seq primer: T7
 Class: BAC ends
 High quality sequence stop: 546.

FEATURES
 source
 1. 546
 Location/Qualifiers

/organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="Plate=812 Col=1 Row=F"
 /clone_lib="RPCI-11 Human Male BAC Library"
 /sex="male"
 /note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI;
 Male blood DNA was isolated from one randomly chosen donor
 and partially digested with a combination of EcoRI and
 EcoRI Methylase. Size selected DNA was cloned into the
 pBAC3.6 vector at EcoRI sites"
 BASE COUNT 135 a 120 c 173 g 108 t 10 others

ORIGIN

Query Match 2.6%; Score 68; DB 17; Length 546;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 372 ATTTCCTGCATGATGCTTCTGAGTCTGTGCTGAGGAACAATGGAAGTCTCCAG 431
 |||||
 DB 383 ATTTCCTGCATGATGCTTCTGAGTCTGTGCTGAGGAACAATGGAAGTCTCCAG 442
 |||||
 OY 432 CAGAAGA 439
 |||||
 DB 443 CAGAAGA 450

RESULT 48
 AG144939/c 701 bp DNA linear GSS 08-JAN-2002
 LOCUS AG144939
 DEFINITION Pan troglodytes DNA, clone: RP43-006B10.T7, genomic survey
 sequence.
 ACCESSION AG144939
 VERSION AG144939.1 GI:16674617
 KEYWORDS GSS.
 SOURCE Pan troglodytes male lymphocytes DNA, clone: RP43-006B10.T7.
 Male BAC library clone: RP43-006B10.T7.

ORGANISM Pan troglodytes
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
 1
 Fujiyama A., Hattori M., Toyoda A., Taylor T.D., Yada T.,
 Toooki Y., Watanabe H. and Sakaki Y.
 BAC end sequences of library RPCI-43
 2 (bases 1 to 701)
 Unpublished

TITLE Fujiyama A., Hattori M., Toyoda A., Taylor T.D., Yada T.,
 Toooki Y., Watanabe H. and Sakaki Y.
 JOURNAL Direct Submission
 Submitted (02-AUG-2001) Aaso Fujiyama, The Institute of Physical
 and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
 1-7-22 Suenhiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 (E-mail:chimbepgsc.riken.go.jp, URL:http://hgp-gsc.riken.go.jp/
 Tel:81-45-503-9111, Fax:81-45-503-9170)
 COMMENT Clones are derived from the chimpanzee BAC library RPCI-43 This BAC
 end was generated during the Red process and may have higher chance
 of clone tracking errors.
 PRIMERS
 Sequencing: T7
 LIBRARY
 Vector : pBAC3.6
 R Site 1 : EcoRI
 R Site 2 : EcoRI

FEATURES
 source
 1. 701
 Location/Qualifiers

/organism="Pan troglodytes"
 /db_xref="taxon:9598"
 /clone="RP43-006B10.T7"
 /sex="male"
 /cell_type="lymphocytes"
 /clone_lib="RPCI-43 Chimpanzee Male BAC Library"
 BASE COUNT 212 a 145 c 159 g 165 t
 ORIGIN

Query Match 2.6%; Score 68; DB 17; Length 701;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2053 AACTCGTACCTGATGATCCACCCAGCTTGGCTCCCAAGTCTGGATTACAGGTG 2112
 |||||
 DB 194 AACTCGTACCTGATGATCCACCCAGCTTGGCTCCCAAGTCTGGATTACAGGTG 135
 |||||
 OY 2113 TGAGCCAC 2120
 |||||
 DB 134 TGAGCCAC 127

RESULT 49
 BG71899/c 742 bp mRNA linear EST 08-MAY-2001
 LOCUS 602699111F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:4831083 5',
 DEFINITION mRNA sequence.
 ACCESSION BG718999
 VERSION BG718999.1 GI:13998186
 KEYWORDS EST
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE 1 (bases 1 to 742)
 NIH-MGC <http://mhc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strauberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
 cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiroki
 Toshiyuki and Piero Carninci (RIKEN)
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LMNL at:
<http://image.lmnl.gov>
 Plate: LMNL0753 row: e column: 04
 High quality sequence stop: 740.
 Location/Qualifiers
 1..742
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:4831083"
 /clone_lib="NIH_MGC_97"
 /lab_host="DH10B"
 /note="Organ: testis; Vector: pBluescript (modified
 pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI (gtcgag
); Oligo-dT primed using primer 5'-TTTTTTTTTTTAA-3',
 size selected for average insert size 2.2 kb and
 normalized to ROT 5. This is a primary library enriched
 for full-length clones and constructed using the
 Cap-trapper method (Carninci, in preparation). Library
 constructed by M. Brownstein (NIH/NHGRI, National
 Institutes of Health). Note: this is a NIH_MGC Library."
 BASE COUNT 232 a 167 c 144 g 199 t
 ORIGIN
 Query Match 2.6%; Score 66; DB 12; Length 742;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2055 CTCCTGACCTCAGGTGATCCACCCAGCTTGCCTCCAAAGTGTGGATTACAGGTGTG 2114
 DB 671 CTCCTGACCTCAGGTGATCCACCCAGCTTGCCTCCAAAGTGTGGATTACAGGTGTG 612
 QY 2115 AGCCAC 2120
 DB 611 AGCCAC 606
 RESULT 50
 A0675390/c 472 bp DNA linear GSS 24-JUN-1999
 LOCUS H8 2151 Al D03 T7C CIR Approved Human Genomic Sperm Library D Homo
 DEFINITION sapiens genomic clone Plate=2151 Col=5 Row=G, DNA sequence.
 ACCESSION A0675390
 VERSION A0675390.1 GI:5208136
 KEYWORDS GSS.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 1 (bases 1 to 472)
 AUTHORS Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
 Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
 Hood, L.
 TITLE Sequence-tagged connectors: A sequence approach to mapping and
 scanning the human genome
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
 MEDLINE 99380589
 COMMENT Contact: Mahairas GG, Wallace JC, Hood L
 High Throughput Sequencing Center
 University of Washington
 401 Queen Anne Avenue North, Seattle, WA 98109, USA
 Tel: (206) 616-3618
 Fax: (206) 616-3887
 Email: jwallace@u.washington.edu
 Clones may be purchased from Research Genetics (info@resgen.com).
 BAC end Web Server: <http://www.htsc.washington.edu>
 Plate: 2151 row: G column: 5
 Seq primer: T7
 Class: BAC ends
 High quality sequence stop: 472.
 Location/Qualifiers
 1..472
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="Plate=2151 Col=5 Row=G"
 /clone_lib="CIR Approved Human Genomic Sperm Library D"
 /sex="male"
 /note="Organ: sperm; Vector: pBelobAC11; BAC Clones in
 E-Coli DH10B"
 BASE COUNT 143 a 73 c 95 g 158 t 3 others
 ORIGIN
 Query Match 2.5%; Score 65; DB 17; Length 472;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2056 TCCGACCTCAGGTGATCCACCCAGCTTGCCTCCAAAGTGTGGATTACAGGTGTGA 2115
 DB 356 TCCGACCTCAGGTGATCCACCCAGCTTGCCTCCAAAGTGTGGATTACAGGTGTGA 297
 QY 2116 GCCAC 2120
 DB 296 GCCAC 292
 RESULT 51
 AUI14545 579 bp mRNA linear EST 05-AUG-2002
 LOCUS AUI14545 HEMBA1 Homo sapiens cDNA clone HEMBA1004880 3', mRNA
 DEFINITION sequence.
 ACCESSION AUI14545
 VERSION AUI14545.1 GI:11006976
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE 1 (bases 1 to 579)
 Oca, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y.,
 Yamamoto, J., Wakamatsu, A., Ozawa, M., Nakamura, Y., Nagai, T., Sugano
 S. and Iwagaki, T.).
 TITLE HRI human cDNA project (Oca, T., Nishikawa, T., Suzuki, Y., Ishii, S.,
 Saito, K., Kawai, Y., Yamamoto, J., Wakamatsu, A., Ozawa, M., Nakamura
 Y., Nagai, T., Sugano, S., Iwagaki, T.)
 JOURNAL Unpublished (2000)
 COMMENT Contact: Takao Iwagaki
 Genomics Laboratory
 Helix Research Institute
 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
 Tel: 81-438-52-3975
 Fax: 81-438-52-3986

Email: genomics@hri.co.jp
 HRI human cDNA project; 5'- & 3'-end one pass sequencing; Helix
 Research Institute; cDNA library construction; Department of
 Virology, Institute of Medical Science, University of Tokyo, and
 Helix Research Institute.

FEATURES

source

1..579
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="HEMBA1004880"
 /clone_1ib="HEMBA1"
 /tissue_type="whole embryo, mainly head"
 /dev_stage="embryo, 10 weeks"
 /note="Vector: pME18SFL3"

BASE COUNT 146 a 133 c 111 g 181 t 8 others
 ORIGIN

Query Match 2.5%; Score 65; DB 9; Length 579;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2056 TCCTGACCTCAGGTGATCCACCCACCTGGCTCCCAAGTCTGGATTACAGGTGTA 2115
 DB 329 TCTGACCTCAGGTGATCCACCCACCTGGCTCCCAAGTCTGGATTACAGGTGTA 388

QY 2116 GCCAC 2120
 DB 389 GCCAC 393

RESULT 52

LOCUS N22395 448 bp mRNA linear EST 20-DEC-1995
 DEFINITION yw31E08.s1 Morton Fetal Cochlea Homo sapiens cDNA clone
 IMAGE:254439 3' similar to contains Alu repetitive element; mRNA
 sequence.

ACCESSION N22395
 VERSION N22395.1 GI:1128529
 KEYWORDS EST

SOURCE

ORGANISM

human.
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

AUTHORS

Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chippelli, B.,
 Chisoso, S., Dietrich, N., Dubuque, T., Pavello, A., Gish, W., Hawkins,
 M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mandis, E., Moore,
 B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T.,
 Schellenberg, K., Soares, M.B., Tan, F., Thierrey-Meg, J., Trevisan, E.,
 Underwood, K., Wohlmann, P., Waterston, R., Wilson, R. and Marra, M.
 Generation and analysis of 280,000 human expressed sequence tags
 Genome Res. 6 (9), 807-828 (1996)

TITLE

JOURNAL

MEDLINE

Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810

Email: est@watson.wustl.edu
 High quality sequence stops: 346
 Source: IMAGE Consortium, LNLN
 This clone is available royalty-free through LNLN; contact the
 IMAGE Consortium (info@image.lnl.gov) for further information.
 Insert length: 844 Std Error: 0.00
 Seq primer: ml3 -40 forward
 High quality sequence stop: 346.

FEATURES

source

1..448
 /organism="Homo sapiens"
 /db_xref="GDB:3891892"
 /db_xref="taxon:9606"
 /clone="IMAGE:254439"
 /clone_1ib="Morton Fetal Cochlea"

/tissue_type="cochlea"
 /dev_stage="16-22 week fetus"
 /lab_host="SOLR cells (kanamycin resistant)"
 /note="Organ: ear; Vector: pBluescript SK-; Site: 1: EcoRI;
 Site 2: XhoI; Reference: Genomics 23, 42-50 (1996) Cloned
 unidirectionally. Primer: Oligo dT. Fetal cochlea, normal.
 37% of inserts < 0.5 kb, 56% 0.5-1.0 kb, 7% > 1 kb. Uni-ZAP
 XR Vector. Library constructed by N. Robertson, C. Morton.
 -5' adaptor sequence: 5' GAATTCGACGAG 3' -3' adaptor
 sequence: 5' CTCGAGTCTTTTCTTTTCTTTT 3' "

BASE COUNT 124 a 105 c 94 g 122 t 3 others
 ORIGIN

Query Match 2.5%; Score 63; DB 14; Length 448;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2058 CTGACCTCAGGTGATCCACCCACCTGGCTCCCAAGTCTGGATTACAGGTGAGC 2117
 DB 214 CTGACCTCAGGTGATCCACCCACCTGGCTCCCAAGTCTGGATTACAGGTGAGC 273

QY 2118 CAC 2120
 DB 274 CAC 276

RESULT 53

LOCUS AO531017 457 bp DNA linear GSS 18-MAY-1999
 DEFINITION RPCI-11-373D14.TV RPCI-11 Homo sapiens genomic clone RPCI-11-373D14
 sequence.

ACCESSION AO531017 GI:4843060
 VERSION AO531017
 KEYWORDS GSS

SOURCE

ORGANISM

human.
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 457)

REFERENCE

AUTHORS

Zhao, S., Adams, M.D., Nierman, W., Malek, J., de Jong, P. and Venter
 'J.C.' BAC End Sequences from Library RPCI-11 for Sequence-Ready
 Map Building (1997)
 Other GSSs: RPCI-11-373D14.TV
 Contact: Shaying Zhao, William Nierman, Mark Adams
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850
 Tel: 301 938 0200
 Fax: 301 938 0208
 Email: hbe@tigr.org

Clones are derived from the human BAC library RPCI-11. For BAC
 library availability, please contact Pieter de Jong
 (pieter@edj.med.buffalo.edu). Clones may be purchased from
 BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
 Research Genes (http://info@resgen.com). BAC end search page:
 http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
 Seq primer: 17
 Class: BAC ends.

FEATURES

source

1..457
 /organism="Homo sapiens"
 /db_xref="GDB:7642933"
 /db_xref="taxon:9606"
 /clone="RPCI-11-373D14"
 /clone_1ib="RPCI-11"
 /sex="Male"
 /cell_type="lymphocytes"
 /note="Vector: pBAC3.6; Site: 1: EcoRI, Site 2: EcoRI;
 RPCI11 Human Male BAC library"

BASE COUNT 127 a 79 c 115 g 136 t

Query Match 2.5%; Score 63; DB 17; Length 457;

Best Local Similarity 100.0%; Fred. No. 0; Mismatches 0; Indels 0; Gaps 0;

Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2058 CTGACCTGAGTATCCACCCACCTGGCTCCCAAGTGTGGATTACAGTGTGAGC 2117

DB 286 CTGACCTGAGTATCCACCCACCTGGCTCCCAAGTGTGGATTACAGTGTGAGC 227

QY 2118 CAC 2120

DB 226 CAC 224

RESULT 54
A0635302
LOCUS
DEFINITION RPT-11-475A11.TV RPT-11 Homo sapiens genomic clone RPT-11-475A11

ACCESSION A0635302
KEYWORDS GSS.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 621)
Zhao, S., Adams, M.D., Nieman, W., Malek, J., de Jong, P. and Venter, J.C.

TITLE Use of BAC End Sequences from Library RPT-11 for Sequence-Ready

JOURNAL Map Building
COMMENT Contact: Shaying Zhao, William Nieman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0200
Email: hbe@tigr.org

Clones are derived from the human BAC library RPT-11. For BAC library availability, please contact Pieter de Jong (pieter@jg.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search.html.
Seq primer: 17
Class: BAC ends.

FEATURES
source location/Qualifiers

1..621
/organism="Homo sapiens"
/db_xref="GDB:7682826"
/db_xref="taxon:9606"
/clone="RPT-11-475A11"
/clone_id="RPT-11"
/sex="Male"
/cell_type="Lymphocytes"
/note="Vector: PBAC3.6; Site 1: EcoRI; Site 2: EcoRI; RPT-11 Human Male Library"

BASE COUNT 132 a 177 c 150 g 162 t
ORIGIN

Query Match 2.5%; Score 63; DB 17; Length 621;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2052 GAATCTGACCTGAGTATCCACCCACCTGGCTCCCAAGTGTGGATTACAGT 2111

DB 222 GAATCTGACCTGAGTATCCACCCACCTGGCTCCCAAGTGTGGATTACAGT 261

QY 2112 GTG 2114

DB 282 GTG 284

RESULT 55
AM859931/c 433 bp mRNA linear EST 19-MAY-2000

LOCUS QV1-CT0364-260100-052-g03 CT0364 Homo sapiens cDNA, mRNA sequence.

DEFINITION AM859931

ACCESSION AM859931.1 GI:7955624

VERSION EST.

KEYWORDS human.

SOURCE Homo sapiens

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 433)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Macskunas, A., Bala, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.U., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil

Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?l=ct2=qv1-CT0364-260100-052-g03&t3=2000-01-26&t4=1)

Seq primer: puc 18 forward

High quality sequence start: 49

High quality sequence stop: 433.

FEATURES
source location/Qualifiers

1..433
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_id="CT0364"
/dev_stage="Adult"

/note="Organ: colon; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORSTES PCR (U.S. Letters Patent application No. 196 716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT 121 a 111 c 108 g 93 t

ORIGIN

Query Match 2.4%; Score 62; DB 10; Length 433;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2059 TGACCTGAGTATCCACCCACCTGGCTCCCAAGTGTGGATTACAGTGTGAGC 2118

DB 171 TGACCTGAGTATCCACCCACCTGGCTCCCAAGTGTGGATTACAGTGTGAGC 112

QY 2119 AC 2120

DB 111 AC 110

RESULT 56
A0343967 543 bp DNA linear GSS 07-MAY-1999

LOCUS RPT-11-112J16.TV RPT-11 Homo sapiens genomic clone RPT-11-112J16,

DEFINITION DNA sequence.

ACCESSION A0343967

VERSION AQ343967.1 GI:4168863
 KEYWORDS GSS.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 543)
 REFERENCE
 AUTHORS Zhao,S., Adams,M.D., Niernan,W., Malek,J., de Jong,P. and Venter
 J.C.
 TITLE Use of BAC End Sequences from library RPCI-11 for Sequence-Ready
 Map Building
 JOURNAL Unpublished (1997)
 COMMENT Other GSSs: RPCI11-112016.TV
 Contact: Shaying Zhao, William Niernan, Mark Adams
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: hbe@igr.org
 Clones are derived from the human BAC library RPCI-11. For BAC
 library availability, please contact Pieter de Jong
 (pieter@dejong.med.buffalo.edu). Clones may be purchased from
 BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
 Research Genetics (http://inforesgen.com). BAC end search page:
 http://www.igr.org/cdb/humgen/bac_end_search/bac_end_search.html
 Seq primer: SP6
 Class: BAC ends.

FEATURES
 source
 1..543
 /organism="Homo sapiens"
 /db_xref="GDB:7542855"
 /db_xref="taxon:9606"
 /clone="RPCI-11-112016"
 /clone_lib="RPCI-11"
 /sex="Male"
 /cell_type="Lymphocytes"
 /note="Vector: pBAC3.6; Site 1: EcoRI; Site 2: EcoRI;
 PCII1 Human Male BAC Library"

BASE COUNT 127 a 138 c 131 g 147 t

ORIGIN

Query Match 2.4%; Score 62; DB 17; Length 543;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2059 TGACCTGAGTGATCCACCACTTGACCTCCCAAGTGTGGATTACAGTGTGAGCC 2118
 |||||
 DB 359 TGACCTGAGTGATCCACCACTTGACCTCCCAAGTGTGGATTACAGTGTGAGCC 418
 |||||

OY 2119 AC 2120
 ||
 DB 419 AC 420

RESULT 57
 AQ435006/c 593 bp DNA linear GSS 31-MAR-1999
 LOCUS HS_5114_B2_A08_T7A RPCI-11 Human Male BAC library Homo sapiens
 DEFINITION genomic clone Plate=690 Col=16 Row=B, DNA sequence.
 ACCESSION AQ435006
 VERSION AQ435006.1 GI:4546345
 KEYWORDS GSS.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 593)
 REFERENCE
 AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
 Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
 Hood,L.
 TITLE Sequence-tagged connectors: A sequence approach to mapping and
 scanning the human genome

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
 MEDLINE 99380589
 COMMENT Contact: Mahairas GG, Wallace JC, Hood L
 High Throughput Sequencing Center
 University of Washington
 401 Queen Anne Avenue North, Seattle, WA 98109, USA
 Tel: (206) 616-3618
 Fax: (206) 616-3887
 Email: jwallace@u.washington.edu
 Clones are derived from the human BAC library RPCI-11. For BAC
 library availability, please contact Pieter de Jong
 (pieter@dejong.med.buffalo.edu). Clones may be purchased from
 BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
 or from Research Genetics (http://inforesgen.com). BAC end web server:
 http://www.hsc.washington.edu
 Plate: 690 row: B column: 16
 Seq primer: 17
 Class: BAC ends
 High quality sequence stop: 593.

FEATURES
 source
 1..593
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="Plate=690 Col=16 Row=B"
 /clone_lib="RPCI-11 Human Male BAC Library"
 /sex="Male"
 /note="Vector: pBAC3.6; Site 1: EcoRI; Site 2: EcoRI;
 Male blood DNA was isolated from one randomly chosen donor
 and partially digested with a combination of EcoRI and
 EcoRI Methylase. Size selected DNA was cloned into the
 pBAC3.6 vector at EcoRI sites"

BASE COUNT 150 a 158 c 117 g 142 t 26 others

ORIGIN

Query Match 2.4%; Score 62; DB 17; Length 593;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2059 TGACCTGAGTGATCCACCACTTGACCTCCCAAGTGTGGATTACAGTGTGAGCC 2118
 |||||
 DB 337 TGACCTGAGTGATCCACCACTTGACCTCCCAAGTGTGGATTACAGTGTGAGCC 278
 |||||

OY 2119 AC 2120
 ||
 DB 277 AC 276

RESULT 58
 AM470105 174 bp mRNA linear EST 24-FEB-2000
 LOCUS x1299g12.x1 NCI-CGAP ut4 Homo sapiens cDNA clone IMAGE:2761606.3
 DEFINITION similar to contains Alu repetitive element; contains element MBR35
 repetitive element; mRNA sequence.
 ACCESSION AM470105
 VERSION AM470105.1 GI:7040211
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 174)
 REFERENCE
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cga@dbp-remail.nih.gov
 Tissue Procurement: Christopher Moskalkuk, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL at:
 www.bio.lnln.gov/bbrp/image/image.html
 Seq primer: 40bp from Gibco
 High quality sequence stop: 137.
 Location/Qualifiers

FEATURES

1..174

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_image="2761606"

/clone_lib="NCI CGAP Ut4"

/tissue_type="serous papillary carcinoma, high grade, 2

pooled tumors

/lab_host="DH10B"

/note="Organ: uterus; Vector: PCMV-SPORT6; Site 1: SalI;

Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.

Average insert size 1.48 kb. Life Technologies catalog #:

11542-016"

BASE COUNT

28 a 45 c 40 g 61 t

ORIGIN

Query Match

Best Local Similarity 100.0%; Pred. No. 0;
 Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2050

TCGAACCTCTGACCTGATGATCCACCCACCTTGCCCTCCCAAGTCTGGATTACAG 2109

Db 51

TCGAACCTCTGACCTGATGATCCACCCACCTTGCCCTCCCAAGTCTGGATTACAG 110

QY 2110

G 2110

Db 111

G 111

RESULT 59

AA748840

LOCUS

AA748840 214 bp mRNA linear EST 16-JAN-1998

DEFINITION

ny76706.s1 NCI CGAP GCB1 Homo sapiens CDNA clone IMAGE:1284227 3'

ACCESSION

AA748840

VERSION

AA748840

KEYWORDS

repetitive element; mRNA sequence.

SOURCE

AA748840.1 GI:2788798

ORGANISM

human.

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

TITLE

1 (bases 1 to 214)
 NCI CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

JOURNAL

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

COMMENT

Tumor Gene Index
 Unpublished (1997)

CONTACT

Contact: Robert Strausberg, Ph.D.

Tissue

Email: cgaabs-remail.nih.gov

Ph.D., Gerald Marti, M.D.

Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,

CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima

Bonaldo, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Found through the I.M.A.G.E. Consortium/LNL at:

www.bio.lnln.gov/bbrp/image/image.html

Seq primer: 40m13 fwd. ET from Amersham

High quality sequence stop: 196.

Location/Qualifiers

1..214

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_image="1284227"

/clone_lib="NCI CGAP GCB1"

/tissue_type="germinal center B cell"

/lab_host="DH10B"

/note="Vector: pT73D-Pac (Pharmacia) with a modified

FEATURES

Location/Qualifiers

1..214

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_image="1284227"

/clone_lib="NCI CGAP GCB1"

/tissue_type="germinal center B cell"

/lab_host="DH10B"

/note="Vector: pT73D-Pac (Pharmacia) with a modified

polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA

was prepared from human tonsillar cells enriched for

germinal center B cells by flow sorting (CD20+, IgD-),

provided by Dr. Louis M. Staudt (NCI), Dr. David Allman

(NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was

primed with a Not I - oligo(dT) primer

15'-GTGTAACATCTGAAGAGGAGGCGCGCTCATTTTCTTTT-3'

(Pharmacia), digested with Not I and Eco RI adaptors

and Eco RI sites of the modified pT73 vector. Library

went through one round of normalization, and was

constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT

42 a 62 c 52 g 58 t

ORIGIN

Query Match

Best Local Similarity 100.0%; Pred. No. 0;
 Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2050

TCGAACCTCTGACCTGATGATCCACCCACCTTGCCCTCCCAAGTCTGGATTACAG 2109

Db 148

TCGAACCTCTGACCTGATGATCCACCCACCTTGCCCTCCCAAGTCTGGATTACAG 207

QY 2110

G 2110

Db 208

G 208

RESULT 60

BI024997/c

LOCUS

BI024997 234 bp mRNA linear EST 14-JUN-2001

DEFINITION

CM4-MT0286-010201-837-d01 MT0286 Homo sapiens CDNA, mRNA sequence.

ACCESSION

BI024997

VERSION

BI024997.1 GI:14431627

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

TITLE

1 (bases 1 to 234)

JOURNAL

Dias Neto E., Garcia Correa R., Verjovski-Almeida S., Briones M.R.,

COMMENT

Nagai M.A., da Silva M. Jr., Zago M.A., Bordin S., Costa F.F.,

CONTACT

Goldman G.H., Carvalho A.F., Matsukuma A., Bala G.S., Simpson D.H.,

Brunstein A., de Oliveira P.S., Bucher P., Jongeneel C.V., O'Hare

M.J., Soares F., Brentani R.R., Reis L.F., de Souza S.J. and

Simpson A.J.

Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

20202663

Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Rui Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?PL=CM4&t=CM4-MT0286-

010201-837-d01&t=32001-02-01&t=4=1)

Seq primer: puc 18 forward

High quality sequence stop: 29

High quality sequence stop: 29

Location/Qualifiers

1..234

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_image="MT0286"

/clone_lib="MT0286"

/dev stage="Adult"

/note="Organ: marrow; Vector: puc18; Site 1: SmaI; Site 2:

SmaI; A mini-library was made by cloning products derived

SmaI; A mini-library was made by cloning products derived

from ORESTES PCR (U.S. Letters Patent application No. 196
'716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."

BASE COUNT 71 a 57 c 62 g 44 t

Query Match 2.4%; Score 61; DB 13; Length 234;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2050 TCGAAGCTCTGAGTGTGATCCACCCAGCTGGCTCCCAAGTCTGGATTACG 2109
Db 182 TCGAAGCTCTGAGTGTGATCCACCCAGCTGGCTCCCAAGTCTGGATTACG 123

OY 2110 G 2110
Db 122 G 122

RESULT 61
BG897239
LOCUS BG897239 309 bp mRNA linear EST 06-NOV-2001
DEFINITION HOA60-1-H3.R HOA (Human Osteoarthritis Cartilage) Homo sapiens cDNA
, mRNA sequence.

ACCESSION BG897239
VERSION BG897239.1 GI:14307480
KEYWORDS EST.

SOURCE human.
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 309)
Kumar, S., Connor, J.R., Dodds, R.A., Halsey, W., Van Horn, M., Mao, J.,
Satche, G., Mui, P., Agarwal, P., Badger, A.M., Lee, J.C., Gowen, M. and
Lack, M.W.

AUTHORS

TITLE Identification and initial characterization of 5000 expressed
sequenced tags (ESTs) each from adult human normal and
osteoarthritic cartilage cDNA libraries

JOURNAL Osteoarthritis. Cartil. 9 (7), 641-653 (2001)

MEDLINE 21482651

COMMENT Contact: Sanjay Kumar
UM2109

GlaxoSmithKline
709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
Tel: 610-270-7245
Fax: 610-270-5598
Email: sanjay.kumar-1@sk.com
Seq primer: F7.

FEATURES

Location/Qualifiers
1..309
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="HOA (Human Osteoarthritis Cartilage)"
/tissue_type="cartilage"
/lab_host="E.coli DH10 B"
/note="Vector: pSPORT 1; Site_1: SalI; Site_2: NotI;
Directional"

BASE COUNT 62 a 93 c 79 g 75 t

ORIGIN

Query Match 2.4%; Score 61; DB 12; Length 309;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2050 TCGAAGCTCTGAGTGTGATCCACCCAGCTGGCTCCCAAGTCTGGATTACG 2109
Db 210 TCGAAGCTCTGAGTGTGATCCACCCAGCTGGCTCCCAAGTCTGGATTACG 269

OY 2110 G 2110
Db 270 G 270

RESULT 62
AA010265
LOCUS AA010265 325 bp mRNA linear EST 09-MAY-1997
DEFINITION 2109605.s1 Soares fetal liver spleen INFUS S1 Homo sapiens cDNA
clone IMAGE:430304 3' similar to contains Alu repetitive element
; contains element MER22 repetitive element ; mRNA sequence.

ACCESSION AA010265
VERSION AA010265.1 GI:1471442
KEYWORDS EST.

SOURCE human.
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 325)
Hallier, L., Lennon, G., Becker, M., Bonaldi, M.F., Chiappelli, B.,
Chissos, S., Dietrich, N., Dubuque, T., Favella, A., Gish, M., Hawkins
'M., Hultman, M., Kucaba, T., Lacy, M., Le, N., Mardis, E., Moore
'B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T.,
Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Treviskis, E.,
Underwood, K., Wohlmann, P., Waterston, R., Wilson, R. and Marra, M.
Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)

AUTHORS

TITLE
JOURNAL
MEDLINE 97044478
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LML; contact the
IMAGE Consortium (info@image.jhmi.gov) for further information.
Insert length: 1517 Std Error: 0.00
Seq primer: mcb.RBGA+ET
High quality sequence stop: 274.

FEATURES

Location/Qualifiers
1..325
/organism="Homo sapiens"
/db_xref="GDB:1330073"
/db_xref="taxon:9606"
/clone_lib="IMAGE:430304"
/clone_lib="Soares_fetal_liver_spleen_INFUS_S1"
/sex="male"
/dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: Liver and Spleen; Vector: p773D (Pharmacia)
with a modified polylinker; Site 1: Pac I; Site 2: Eco RI;
This is a subtracted version of the original Soares fetal
liver spleen INFUS library. 1st strand cDNA was primed
with a Pac I - oligo(dT) primer [5',
AACGTGAGATTTATTAAGATCTTTTCTTTTCTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Pac I and cloned into the Pac I
and Eco RI sites of the modified p773 vector. Library
went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Bonaldi."

BASE COUNT 69 a 92 c 66 g 97 t 1 others

ORIGIN

Query Match 2.4%; Score 61; DB 9; Length 325;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2050 TCGAAGCTCTGAGTGTGATCCACCCAGCTGGCTCCCAAGTCTGGATTACG 2109
Db 168 TCGAAGCTCTGAGTGTGATCCACCCAGCTGGCTCCCAAGTCTGGATTACG 227

OY 2110 G 2110
Db 228 G 228


```

RESULT 63
AA993165      346 bp mRNA linear EST 27-AUG-1998
LOCUS         oc77c09.s1 Soares_tetuc_Nb2HF8_9w Homo sapiens cDNA clone
DEFINITION   IMAGE:1622800 3' similar to contains Alu repetitive element; mRNA
sequence.
ACCESSION    AA993165
VERSION      AA993165.1 GI:3179710
KEYWORDS     EST.
SOURCE       human.
ORGANISM     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE    1 (bases 1 to 346)
AUTHORS      NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE        National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
JOURNAL      Tumor Gene Index
COMMENT      Unpublished (1997)
              Contact: Robert Strausberg, Ph.D.
              Email: cga@bbs-remail.nih.gov
              This clone is available royalty-free through LNL; contact the
              IMAGE Consortium (info@image.llnl.gov) for further information.
              Insert Length: 1727 Std Error: 0.00
              Seq primer: -40m13 fwd. RT from Amersham
              High quality sequence stop: 338.
              Location/Qualifiers
                1..346
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone="IMAGE:1622800"
                /clone_1ib="Soares_tetuc_Nb2HF8_9w"
                /dev_stage="8-9 weeks"
                /lab_host="MDH10B"
                /note="vector: pT73D-Pac (Pharmacia) with a modified
                polylinker. Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                was prepared from mRNA obtained from pooled 8-9 week
                (total) fetus material with a Not I - oligo(dT) primer [5'
                TGTTACCACTCTGAGAGCGAGCGCGCTTAATTTTATTTTATTTT 3'].
                Double-stranded cDNA was ligated to Eco RI adaptors
                (Pharmacia), digested with Not I and cloned into the Not I
                and Eco RI sites of the modified pT73D vector. Library
                went through one round of normalization, and was
                constructed by Bento Soares and M. Fatima Bonaldo. "

BASE COUNT   78 a 94 c 75 g 99 t

ORIGIN
Query Match 2.4%; Score 61; DB 9; Length 346;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2050 TCGAAGCTCTGACCTGAGTGATCCACCCCTTGCCCTCCCAAGTGTGGATTACAG 2109
|||||
Db 204 TCGAAGCTCTGACCTGAGTGATCCACCCCTTGCCCTCCCAAGTGTGGATTACAG 263

QY 2110 G 2110

Db 264 G 264

RESULT 64
AV762430/3 350 bp mRNA linear EST 19-OCT-2000
LOCUS         AV762430 MDS Homo sapiens cDNA clone MDSBF09 5', mRNA sequence.
DEFINITION   AV762430
ACCESSION    AV762430
VERSION      AV762430.1 GI:10920278
KEYWORDS     EST.
SOURCE       human.
ORGANISM     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE    1 (bases 1 to 350)
AUTHORS      Gu, Y., Zhao, M., Huang, Q., Xu, X., Li, Y., Peng, Y., Song, H., Xiao, H.,
              Gu, Y., Li, N., Qian, B., Liu, F., Qu, J., Gao, X., Cheng, Z., Xu, Z., Zeng

FEATURES
source
1..377
/organism="Homo sapiens"

TITLE
JOURNAL
COMMENT
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203 P. R. China
Tel: 86-21-50801919 (ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.
Location/Qualifiers
  1..350
  /organism="Homo sapiens"
  /db_xref="taxon:9606"
  /clone="MDSBF09"
  /clone_1ib="MDS"
  /tissue_type="Bone marrow"
  /cell_type="CD34+ hematopoietic stem/progenitor cell"
  /lab_host="BM25.8"
  /note="vector: pT73D-Pac; Site_1: SfiI; Site_2: SfiI"

BASE COUNT   93 a 86 c 100 g 71 t

ORIGIN
Query Match 2.4%; Score 61; DB 10; Length 350;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2050 TCGAAGCTCTGACCTGAGTGATCCACCCCTTGCCCTCCCAAGTGTGGATTACAG 2109
|||||
Db 80 TCGAAGCTCTGACCTGAGTGATCCACCCCTTGCCCTCCCAAGTGTGGATTACAG 21

QY 2110 G 2110

Db 20 G 20

RESULT 65
AA731898      377 bp mRNA linear EST 07-FEB-1998
LOCUS         nw77d10.s1 NCI CGAP_CG01 Homo sapiens cDNA clone IMAGE:1252051 3'
DEFINITION   similar to contains Alu repetitive element; contains element PTR5
sequence.
ACCESSION    AA731898
VERSION      AA731898.1 GI:2752709
KEYWORDS     EST.
SOURCE       human.
ORGANISM     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE    1 (bases 1 to 377)
AUTHORS      NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE        National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
JOURNAL      Tumor Gene Index
COMMENT      Unpublished (1997)
              Contact: Robert Strausberg, Ph.D.
              Email: cga@bbs-remail.nih.gov
              Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
              Ph.D., Gerald Marti, M.D.
              cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
              Bonaldo, Ph.D.
              cDNA Library Arrayed by: Greg Lennon, Ph.D.
              DNA Sequencing by: Washington University Genome Sequencing Center
              Clone distribution: NCI-CGAP clone distribution information can be
              found through the I.M.A.G.E. Consortium/LNL at:
              www.bio.llnl.gov/dbp/image/image.html
              Insert Length: 1654 Std Error: 0.00
              Seq primer: -40m13 fwd. RT from Amersham
              High quality sequence stop: 376.
              Location/Qualifiers
                1..377
                /organism="Homo sapiens"

```

/db_xref="taxon:9606"
 /clone="IMAGE:1252051"
 /clone_lib="NCI CGAP GCBI1"
 /tissue_type="germinal center B cell"
 /lab_host="DH10B"
 /note="Vector: pUT3D-Pac (Pharmacia) with a modified polylinker. Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was prepared from human tonsillar cells enriched for germinal center B cells by flow sorting (CD20+, IgD-), provided by Dr. Louis M. Staudt (NCI), Dr. David Allman (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was primed with a Not I - oligo (dT) primer [5'-TGTTACCAATCTGAGTGCAGCCGCGCCCTCATTTTCTTTT-3']. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pUT3D vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 86 a 103 c 73 g 115 t

ORIGIN

Query Match 2.4%; Score 61; DB 9; Length 377;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2050 TCGAATCTGAGTGCAGTGCAGCCGCGCCCTCATTTTCTTTT-3'
 |||
 DB 148 TCGAATCTGAGTGCAGTGCAGCCGCGCCCTCATTTTCTTTT-3'

OY 2110 G 2110
 DB 208 G 208

RESULT 66
 LOCUS BF431825 405 bp mRNA linear EST 19-JAN-2001
 DEFINITION nabs0n08.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3269606.3, similar to contains Alu repetitive element ; contains element MER22 repetitive element ;, mRNA sequence.

ACCESSION BF431825.1 GI:11443939
 VERSION EST.

KEYWORDS human.

SOURCE

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 405)
 NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapdb-remail.nih.gov

This clone is available royalty-free through INLIL; contact the IMAGE Consortium (info@image.lilil.gov) for further information.
 Seq primer: -40UP from Gibco
 High quality sequence stop: 385.

FEATURES

source 1. .405
 Location/Qualifiers

/organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:3269606"
 /clone_lib="Soares_NSF_F8_9W_OT_PA_P_S1"
 /lab_host="DH10B"

/note="Organ: pooled; Vector: pUT3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from five normalized libraries were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 5 libraries. The pools consisted of the following

libraries and clones: Soares NBHP pool 1: 399384-310919, 323208-325895 Soares NBHP pool 1: 15032-14735, 147720-148103, 146872-149255, 15002 - 150407, 151176-152327 Soares NBHP pool 1: 758280-760583, 772104-774407 Soares NBHP pool 1: 304776-306311, 320136-322823, 326280-326663 Soares NBHP pool 1: 723720-726407, 739080-740999 Subtraction by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 83 a 113 c 84 g 125 t

ORIGIN

Query Match 2.4%; Score 61; DB 12; Length 405;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2050 TCGAATCTGAGTGCAGTGCAGCCGCGCCCTCATTTTCTTTT-3'
 |||
 DB 207 TCGAATCTGAGTGCAGTGCAGCCGCGCCCTCATTTTCTTTT-3'

OY 2110 G 2110
 DB 267 G 267

RESULT 67
 LOCUS BE169632 412 bp mRNA linear EST 21-JUN-2000
 DEFINITION PM-H70527-280200-005-b12 HT0527 Homo sapiens cDNA, mRNA sequence.

ACCESSION BE169632
 VERSION BE169632.1 GI:8632353

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 412)
 Dias Neto E., Garcia Correa R., Verjovski-Almeida S., Briones M.R., Nagai M.A., da Silva W. Jr., Zago M.A., Bordin S., Costa F.F., Goldman G.H., Carvalho A.F., Matsukuma A., Bala G.S., Simpson D.H., Brunstein A., de Oliveira P.S., Bucher P., Jongeneel C.V., O'Hare M.J., Soares F., Brentani R.R., Reis L.F., de Souza S.J. and Simpson A.J

Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

TITLE

JOURNAL

MEDLINE

COMMENT

Contact: Simpson A.J.G., Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil

Tel: +55-11-2704922
 Fax: +55-11-2707001

Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?l=ht2=PM-H70527-280200-005-b12&t=3200-02-28&t4=1)

Seq primer: puc 18 forward
 High quality sequence start: 27
 High quality sequence stop: 216.

Location/Qualifiers

1. .412

/organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="PM-H70527"

/dev_stage="Adult"

/note="Organ: head; neck; Vector: puc18, Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORFESTS PCR (U.S. letters patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under

libraries and clones: Soares NBHP pool 1: 399384-310919, 323208-325895 Soares NBHP pool 1: 15032-14735, 147720-148103, 146872-149255, 15002 - 150407, 151176-152327 Soares NBHP pool 1: 758280-760583, 772104-774407 Soares NBHP pool 1: 304776-306311, 320136-322823, 326280-326663 Soares NBHP pool 1: 723720-726407, 739080-740999 Subtraction by Bento Soares and M. Fatima Bonaldo."

TITLE
Quackenbush, J.
Assessment of gene expression patterns in a model of colon tumor metastasis using a 19,200 element cDNA microarray
Unpublished (2000)
COMMENT
Contact: John Quackenbush
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3528
Fax: 301 838 0208
Email: johnq@igr.org
Plate: 286
Seq primer: Forward.

FEATURES
source
1. .501
Location/Qualifiers

BASE COUNT
119 a 128 c 150 g 104 t
ORIGIN
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="MAGE resequences, MAGI"
/note="Vector: pBluescriptSkm"

Query Match
Best Local Similarity 100.0%; Pred. No. 0;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2050 TCGAAGCTCTGACCTGAGTATCCACCCAGCTTGGCTCCCAAGTGGGATTACAG 2109
Db 188 TCGAAGCTCTGACCTGAGTATCCACCCAGCTTGGCTCCCAAGTGGGATTACAG 129

Qy 2110 G 2110
Db 128 G 128

RESULT 73
AW753552 568 bp mRNA linear EST 28-APR-2000
LOCUS
DEFINITION PM3-CT0264-151099-001-g05 CT0264 Homo sapiens cDNA, mRNA sequence.
ACCESSION
AW753552
VERSION
AW753552.1 GI:7668484
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE
1 (bases 1 to 568)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagal, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare
, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?fl=PM3&ct2=PM3-CT0264-
151099-001-g05&ct3=1999-10-15&ct4=1)
Seq primer: puc 18 forward
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Location/Qualifiers

source

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Sma1; A mini-library was made by cloning products derived
from ORESTES PER (U.S. Letters Patent application No. 196
, 716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."
BASE COUNT
140 a 118 c 112 g 198 t
ORIGIN

Query Match
Best Local Similarity 100.0%; Pred. No. 0;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2050 TCGAAGCTCTGACCTGAGTATCCACCCAGCTTGGCTCCCAAGTGGGATTACAG 2109
Db 164 TCGAAGCTCTGACCTGAGTATCCACCCAGCTTGGCTCCCAAGTGGGATTACAG 223

Qy 2110 G 2110
Db 224 G 224

RESULT 74
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LOCUS
DEFINITION MR0-ST0020-201099-003-b12 ST0020 Homo sapiens cDNA, mRNA sequence.
ACCESSION
AW806847
VERSION
AW806847.1 GI:7899841
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE
1 (bases 1 to 613)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagal, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare
, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?fl=MR0-ST0020-201
099-003-b12&ct3=1999-10-20&ct4=1)
Seq primer: puc 18 forward
High quality sequence start: 47
High quality sequence stop: 594.
Location/Qualifiers

TITLE
JOURNAL
MEDLINE
COMMENT

FEATURES
source

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Site 2: Sma1; A mini-library was made by cloning products

FEATURES

Tue Apr 1 06:01:17 2003

us-09-988-971-1.oligo.rst

Page 38

derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT 142 a 149 c 193 g 129 t

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OY 2112 G 2112
Db 373 G 373

RESULT 75
AV733872/c 618 bp mRNA linear EST 17-OCT-2000

LOCUS AV733872
DEFINITION AV733872 cda Homo sapiens cDNA clone cdaASG06 5', mRNA sequence.
ACCESSION AV733872
VERSION AV733872.1 GI:10851417
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE
AUTHORS Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
1 (bases 1 to 618)
Yang, Y., Song, H., Peng, Y., Gu, Y., Gao, G., Xiao, H., Xu, X., Li, N.,
Qian, B., Liu, F., Ou, J., Gao, X., Cheng, Z., Xu, Z., Zeng, L., Xu, S., Gu,
W., Yu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu, G., Hu, R., Chen, J.,
Chen, Z. and Han, Z.
Homo sapiens cDNA clones
Unpublished (2000)

TITLE
JOURNAL
COMMENT Chinese National Human Genome Center at Shanghai
Contact: Zeguang Han
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919 (ex. 45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.

FEATURES
source
1..618
Location/Qualifiers

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OY 2110 G 2110
Db 503 G 503

Search completed: March 30, 2003, 19:49:22
Job time: 4114 secs